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Applicants: Hans Christian Thøgersen, Ristrupvej 41, 8381 Mundelstrup, DK; Michael Etzerodt, Mosevænget 5, 8382 Hinnerup, DK; Thor Las Holtet, 13, Mortimer Road, Royston, Hertfordshire SG8 7HS, GB; Niels Jonas Heilskov Graversen, Brendstrupvej 58, 8200 Aarhus N, DK; Jette Sandholm Kastrup, Tokkekøbvej 6, 3450 Allerød, DK; Bettina Bryde Nielsen, Strøhusvej 76.D, 2670 Greve, DK; Ingrid Kjøller Larsen, Ingersvej 23, 2920 Charlottenlund, DK

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Lizzi Vester

Lizzi Vester
Afdelingsleder

FIELD OF THE INVENTION

The present invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family, and their use in rational *de novo* design and production of multi-functional molecules.

BACKGROUND OF THE INVENTION

Tetranectin is a Ca^{2+}-binding trimeric C-type lectin which is present in blood plasma and from the extracellular matrix of certain tissues. The tetranectin group of proteins comprises tetranectin isolated from man and from mouse and the highly related C-type lectin homologues isolated from the cartilage of cattle (Neame and Boynton, database accession number PATCHX:u22298) and from reef shark (Neame *et al.*, 1992, Neame *et al.*, 1996 and database accession number p26258 and PIR2:A37289).

The mature tetranectin polypeptide chain of 181 amino acid residues is encoded in three exons as shown by molecular cloning and characterisation of the gene (Berglund & Petersen, 1992; Wewer & Albrechtsen, 1992). Exon 3 of the human tetranectin gene encodes a separate functional and structural unit, a single long-form so-called carbohydrate recognition domain (CRD), with three intra-chain disulphide bridges. The tetranectin CRD is considered to belong to a distinct class of C-type lectins (Day, 1994) clearly related to C-type lectins by sequence homology, conservation of disulphide topology (Fuhlendorff *et al*, 1987) and by the presence of an almost conserved suit of amino acid residues known to be involved in binding of calcium ions.

A published poster (Holtet *et al* 1996) has proposed tetranectin to be a trimer and that trimerisation is governed by the peptide encoded by exon 1. The peptide encoded by exon 1 was proposed to be "necessary and sufficient to govern trimerisa-

tion" whereas the polypeptide encoded by exon 2 was proposed as being "involved in lysine-sensitive binding to plasminogen".

SUMMARY OF THE INVENTION

It has surprisingly been found by the present inventors that the human tetranectin polypeptide (and derivatives thereof) is capable of forming very stable trimers which have a number of advantageous characteristics and uses. Notably, the tetranectin molecule includes a trimerising structural element which can be used as carrier of other chemical entities, thereby providing a carrier molecule of a hitherto unseen versatility.

Prior published knowledge in the field of providing trimerising polypeptides of choice includes the disclosure in WO 95/31540 by Hoppe and Reid which describes a trimerisation module derived from collectin coiled coil structures and its application in engineering of artificially trimerised proteins. Several interesting areas of application are common to that patent publication and to the present disclosure. However, in several ways the properties of the trimerisation modules derived from the tetranectin protein family as disclosed herein are markedly different in fundamental architecture and represent surprisingly improved properties in comparison with the collectin trimerisation unit:

(1) Although the spatial structures of both trimerisation modules at a superficial level appear as similar in that both are ternary coiled coil structures of roughly equivalent spatial size the structural basis for adopting this spatial configuration is markedly distinct between the two groups of proteins. In fact, it is so distinct that the common belief prior to the work of Holtet *et al.* on cross-linking of human tetranectin (Holtet *et al.*, 1996) was that this family of proteins were tetrameric (hence the name). Accordingly, the sequences of the tetranectin family of trimerisation modules

does not conform to the declared common motif delineated for the collectin family (WO 95/31540, page 8).

(2) The thermal stability of the tetranectin trimerisation module (as shown in the examples) is such that the trimer can be shown to exist even at about 60°C (Example 4, trimerised tetranectin) or at about 70°C (Example 3, trimerised ubiquitin), whereas a collectin trimer unit falls apart at about 50-55°C (WO 95/31540, Example 1, page 36 therein).

(3) Whereas it remains uncertain whether the collectin trimerisation domain possibly allows attachment of fusion partners at C-terminal ends of the trimerisation module, and whereas no example has been reported of successful or claimed successful attachment of a foreign protein (except for the GST fusion partner) to the N-terminal region of the collectin trimerisation module, the information disclosed herein demonstrates that the tetranectin trimerisation module is more versatile in that is allows attachment of foreign proteins to either, as well as to both, terminus or termini simultaneously (Examples 1-4). This has important consequences as the tetranectin trimerisation module may be deployed to construct molecules that are able to interact (each end with a binding valency up to 3) simultaneously with two bulky interaction partners like e.g. cell surfaces.

(4) The virtual absence of subunit exchange between monomers of a trimer that has been trimerised using the tetranectin trimerisation modules disclosed herein is by first principles of thermodynamics correlated with the surprisingly high thermal stability of the complex. It will hence be apparent that the advantages inherent to the "pick-and-mix" applications of the technology, as disclosed herein, may be used to much greater advantage because of the much longer shelf life expected for the heterofunctional products of the present invention.

The polypeptide constructs CIIH6FXTN123, H6FXTN123, H6FXTN12, and H6FXTN23 which all involve parts of the tetranectin molecule have previously been prepared (cf. e.g. WO 94/18227) but these constructs have all been provided with a view to facilitating expression and/or purification of the tetranectin derived moiety of the constructs. To the best of the inventors' knowledge no publications exist which reports any use of tetranectin derivatives as "building blocks" to which other chemical moieties advantageously could be coupled.

Hence, in its broadest aspect the present invention relates to a monomer polypeptide construct comprising at least one tetranectin trimerising structural element (hereinafter designated a TTSE) which is covalently linked to at least one heterologous moiety, said TTSE being capable of forming a stable complex with two other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23, the sequences of which are shown in SEQ ID NOs: 24-27. It is preferred that the heterologous moiety is one which does not exclusively facilitate expression and/or purification of the monomer polypeptide construct.

The invention further relates to oligomeric molecules comprised of at least two of such monomer polypeptide constructs, and the invention also relates to methods of preparing the monomer polypeptide constructs and the oligomers. The invention further relates to a kit comprising monomer polypeptide constructs in separate packages, ready for use in a "pick-and-mix" approach for use of the monomers. Finally, the invention also pertains to fragments which include nucleic acid sequences which encode the monomer polypeptide constructs, as well as to vectors and cells containing these nucleic acid fragments.

LEGENDS TO THE FIGURES

Fig. 1: Amino acid sequence of the amino terminal region of tetranectin.
Amino acid sequence (in one letter code) from E1 to L51 of tetranectin (SEQ ID NO: 7). Exon 1 comprises residues E1 to D16 and exon 2 residues V17 to V49, respectively. The alpha helix extends beyond L51 to K52 which is the C-terminal amino acid residue in the alpha helix.

Fig. 2: Alignment of the amino acid sequences of the trimerising structural element of the tetranectin protein family.
Amino acid sequences (one letter code) corresponding to residue V17 to K52 comprising exon 2 and the first three residues of exon 3 of human tetranectin (SEQ ID NO: 7); murine tetranectin (Sørensen et al., Gene, 152: 243 -245, 1995); tetranectin homologous protein isolated from reef-shark cartilage (Neame and Boynton, 1992,1996); and tetranectin homologous protein isolated from bovine cartilage (Neame and Boynton, database accession number PATCHX:u22298). Residues at a and d positions in the heptad repeats are listed in boldface. The listed consensus sequence of the tetranectin protein family trimerising structural element comprise the residues present at a and d positions in the heptad repeats shown in the figure in addition to the other conserved residues of the region. "hy" denotes an aliphatic hydrophobic residue.

Fig. 3: Construction of the expression plasmids pTH6FXtripa and pTH6FXtripb.
The amplified DNA fragments tripa and tripb harbouring the tetranectin amino acid sequence (SEQ ID NO: 7) from E1 to T48 and E1 to K52, respectively, fused in the 5' end to nucleotide sequences encoding a FX_a cleavage site IQGR (SEQ ID NO: 4) and the recognition sites for the restriction endonucleases BglII and KpnI, were cut with the restriction enzymes BclI and HindIII and ligated into the BamHI and

HindIII sites of the expression plasmid pT7H6 (Christensen et al., 1991) using standard procedures.

Fig. 4: Predicted amino acid sequence of the fusion proteins H6FXtripa (SEQ ID NO: 28) and H6FXtripb (SEQ ID NO: 29) encoded by the expression plasmids pTH6FXtripa and pTH6FXtripb, respectively.

Fig. 5: Construction of the expression plasmids pTH6FXTN123 and pTCIIH6FXTN123.
The amplified DNA fragment corresponding to the full length, mature tetranectin monomer (SEQ ID NO: 7) from E1 to V181 fused in the 5' end to nucleotide sequences encoding a FX_a cleavage site IEGR (SEQ ID NO: 10) was cut with the restriction enzymes BamHI and HindIII and ligated into the corresponding sites of the expression plasmids pT7H6 (Christensen et al., 1991) and pTCIIH6 using standard procedures. pTCIIH6 was derived from pT7H6 by substitution of the NdeI - HindIII fragment of pT7H6 with the NdeI - HindIII fragment of pLcII (Nagai and Thøgersen, 1987) encoding the first 32 residues of the lambda cII protein MVRANKRNEALRIESALLNKIAMLGTEKTAEG (SEQ ID NO: 11) fused in the 3' end to a nucleotide sequence encoding the H6 sequence GSHHHHHHGS(SEQ ID NO: 12).

Fig. 6: Predicted amino acid sequence of the fusion proteins H6FXTN123 (SEQ ID NO: 25) and CIIH6FXTN123 (SEQ ID NO: 24) encoded by the expression plasmids pTH6FXTN123 and pTCIIH6FXTN123, respectively.

Fig. 7: Construction of the expression plasmids pTH6FXTN12, pTH6FXTN23, and pTH6FXTN3.
The amplified DNA fragments corresponding to the tetranectin derivatives TN12 and TN3 from E1 to V49 and A45 to V181, respectively (SEQ ID NO: 7) fused in the 5' end to nucleotide sequences encoding the FX_a cleavage site IEGR (SEQ ID NO: 10) was cut with the restriction enzymes BamHI and HindIII and ligated into the corresponding sites of the expression plasmids pT7H6 (Christensen et al., 1991) using standard pro-

cedures. The amplified DNA fragment corresponding to the tetranectin derivative TN23 from V17 to V181 (SEQ ID NO: 7) fused in the 5' end to nucleotide sequences encoding the FX_a cleavage site IQGR (SEQ ID NO: 4) was cut with the restriction enzymes BamHI and HindIII and ligated into the corresponding sites of the expression plasmids pT7H6 (Christensen et al., 1991) using standard procedures.

Fig. 8: Predicted amino acid sequence of the fusion proteins H6FXTN12 (SEQ ID NO: 26), H6FXTN23 (SEQ ID NO: 27), and H6FXTN3 (SEQ ID NO: 30) encoded by the expression plasmids pTH6FXTN12, pTH6FXTN12, respectively.

Fig. 9: Gel filtration analysis of TN123, TN23, and TN3 Analytical gel filtration of the recombinant tetranectin derivatives TN123, TN23, and TN3 were performed on a Superose 12 HR 10/30 column (Pharmacia, Sweden) with a total volume of 25 ml in 100 mM NaCl and 50 mM Tris-HCl pH 8 and a flow rate of 0.2 ml/min. Vertical bars at peak maxima identify elution profiles for each of the three proteins.

Fig. 10: Cross-linking analysis of TN123 and CIIH6FXTN123. Samples of TN123, CIIH6FXTN123 and mixtures of both were incubated with DMSI and analyzed by SDS-PAGE (12% gel). Before addition of DMSI, protein mixtures were subjected to subunit exchange by incubation at 70°C for varying length of time. Protein marker of 94, 68, 43 and 30 kDa, top to bottom (lane M). CIIH6FXTN123 fusion protein (lane 1). TN123 (lane 2). DMSI treated CIIH6FXTN123 (lanes 3 and 6). DMSI-treated TN123 (lane 4). Identical samples of DMSI treated mixtures of CIIH6FXTN123 and TN123 without heat exposure (lanes 5 and 7) and heat treated for 2.5 sec, 15 sec, 2.5 min. and 10 min., respectively, before treatment with DMSI (lanes 8-11).

Fig. 11: Cross-linking analysis of the recombinant tetranectin derivatives TN123, TN23, TN3, and H6FXTN12.
The recombinant proteins TN123, TN23,TN3, H6FXTN12 or mixtures of TN123 and each of the other were analyzed by SDS-

PAGE. Protein marker of 94, 68, 43, 30, 20, and 14.4 kDa, top to bottom (lane M). TN123 cross-linked with DMSI (lane 1). TN123 and H6-rTN12 cross-linked with DMSI without and with heat treatment at 70°C for two min. (lanes 2 and 3). H6FXTN12 cross-linked with DMSI (lanes 4 and 5). Mixture of TN123 and H6FXTN12, no cross-linking (lane 6). Cross-linking of TN123 and TN23 without and with heat treatment at 70°C for two min. (lanes 7 and 8). Cross-linking of TN23 (lane 9). Mixture of TN123 and TN23 without cross-linking (lane 10). TN123 cross-linked by DMSI (lane 11). Cross-linking of TN123 and TN3 without and with heat treatment for two min. (lanes 12 and 13). Cross-linking of TN3 (Lane 14). Mixture of TN123 and TN3, no cross-linking (lane 15).

Fig. 12: Cross-linking based analysis of the trimer thermal stability.
In parallel experiments TN123 and the fusion protein H6FXtripb-UB (SEQ ID NO: 31) were cross-linked with DMSI at different temperatures and the samples analyzed by SDS-PAGE. Protein marker of 94, 68, 43, 30, 20, and 14.4 kDa, top to bottom (lane M). TN123 without cross-linking (lane 1). TN123 cross-linked with DMSI for 15 min. at 37°C, 50°C, 60°C, and 70°C (lanes 2 to 5), respectively. The fusion protein H6FXtripb-UB (SEQ ID NO: 31) without cross-linking (lane 6). H6FXtripb-UB cross-linked with DMSI for 15 min. at 37°C, 50°C, 60°C, and 70°C (lanes 7 to 10), respectively and H6FXtripb-UB incubated at 70°C for 15 min. (lane 11).

Fig. 13: Construction of the expression plasmid pTH6FXtripb-UB.
The amplified DNA fragment comprising the nucleotide sequence (SEQ ID NO:16) encoding the ubiquitin amino acid sequence (SEQ ID NO: 19) from Q2 to G76 was cut with the restriction enzymes BclI and HindIII and ligated into the BamHI and HindIII sites of the expression plasmid pT7H6FXtripb (Example 1) using standard procedures.

Fig. 14: Predicted amino acid sequence of the fusion protein H6FXtripb-UB (SEQ ID NO: 31) encoded by the expression plasmid pTH6FXtripb-UB.

Fig. 15: Construction of the expression plasmid pTH6FXscFV (CEA6)tripb.
The DNA fragment, amplified with the primer pair SEQ ID NOs: 21 and 22, comprising the nucleotide sequence SEQ ID NO: 20 encoding the single chain antibody CEA6, scFV (CEA6), amino acid sequence from Q1 to A261 was cut with the restriction enzymes BamHI and KpnI and ligated into the BglII and KpnI sites of the expression plasmid pT7H6FXtripb (Example 1) using standard procedures.

Fig. 16: Predicted amino acid sequence of the fusion protein H6FXscFV(CEA6)tripb encoded by the expression plasmid pH6FXscFV(CEA6)tripb.

Fig. 17: Construction of the expression plasmid pTH6FXtripbscFX(CEA6).
The DNA fragment, amplified with the primer pairs having SEQ ID NO: 21 and 23, comprising the nucleotide sequence (SEQ ID NO: 20) encoding the single chain antibody CEA6, scFV (CEA6), amino acid sequence from Q1 to A261 was cut with the restriction enzymes BamHI and HindIII and ligated into the BamHI and HindIII sites of the expression plasmid pT7H6FXtripb (Example 1) using standard procedures.

Fig. 18: Predicted amino acid sequence of the fusion protein H6FXtripbscFv(CEA6) encoded by the expression plasmid pH6FXtripbscFv(CEA6).

Fig. 19: Construction of the expression plasmid pTH6FXscFv(CEA6)tripbscFX(CEA6).
The DNA fragment, amplified with the primer pair SEQ ID NO: 21 and 23, comprising the nucleotide sequence (SEQ ID NO: 20) encoding the single chain antibody CEA6, scFV (CEA6), amino acid sequence from Q1 to A261 was cut with the restriction

enzymes BamHI and HindIII and ligated into the BamHI and HindIII sites of the expression plasmid pT7H6FXscFv(CEA6)tripb (Example 4) using standard procedures.

Fig. 20: Predicted amino acid sequence of the fusion protein H6FXscFv(CEA6)tripbscFv(CEA6) (SEQ ID NO: 34) encoded by the expression plasmid pH6FXscFv(CEA6)tripbscFv(CEA6).

Fig. 21: Cross-linking analysis of the H6FXtripbscFv(CEA6) fusion protein (SEQ ID NO: 33).
In parallel experiments the fusion proteins H6FXtripbscFv(CEA6) (SEQ ID NO: 33) and TN123 were cross-linked at room temperature for 30 min. with 0 mg/ml, 0.5 mg/ml, 1.0 mg/ml, 1.5 mg/ml, and 2.0 mg/ml of DMSI, respectively. Lane 1: H6FXtripbscFv(CEA6) without DMSI, H6FXtripbscFv(CEA6) with 0.5 mg/ml DMSI (lane 2), H6FXtripbscFv(CEA6) with 1.0 mg/ml DMSI (lane 3), H6FXtripbscFv(CEA6) with 1.5 mg/ml DMSI (lane 4) and H6FXtripbscFv(CEA6) with 2.0 mg/ml DMSI (lane 5). Protein marker of 94, 68, 43, 30, 20, and 14.4 kDa, top to bottom (lane M). Lane 6: TN123 without DMSI, TN123 with 0.5 mg/ml DMSI (lane 7), TN123 with 1.0 mg/ml DMSI (lane 8) TN123 with 1.5 mg/ml DMSI (lane 9) and TN123 with 2.0 mg/ml DMSI (lane 10).

DETAILED DISCLOSURE OF THE INVENTION

The term "trimerising structural element" (TTSE) used in the present description and claims is intended to refer to the portion of a polypeptide molecule of the tetranectin family which is responsible for trimerisation between monomers of the tetranectin polypeptide. The term is also intended to embrace variants of a TTSE of a naturally occurring tetranectin family member, variants which have been modified in the amino acid sequence without adversely affecting, to any substantial degree, the trimerisation properties relative to those of the native tetranectin family member molecule. Specific examples of such variants will be described in

detail herein, but it is generally preferred that the TTSE is derived from human tetranectin, murine tetranectin, C-type lectin of bovine cartilage, or C-type lectin of shark cartilage. Especially preferred is monomer polypeptide constructs including at least one TTSE derived from human tetranectin.

The 49 residue polypeptide sequence encoded by exons 1 and 2 of tetranectin (Fig. 1) appears to be unique to the tetranectin group of proteins (Fig. 2) as no significant sequence homology to other known polypeptide sequences has been established. In preparation for experimental investigations of the architecture of tetranectin a collection of recombinant proteins was produced, the collection including complete tetranectin, the CRD domain (approximately corresponding to the polypeptide encoded by exon 3), a product corresponding to the polypeptide encoded by exons 2+3, a product corresponding to exons 1+2 (Holtet *et al.*, 1996; Example 2). As detailed in Example 2 we now know differently: tetranectin is indeed a trimer, but the exon 2 encoded polypeptide is in fact capable of effecting trimerisation by itself as evidenced by the observation that the recombinant protein corresponding to exons 2+3 is in fact trimeric in solution.

3D-structure analysis of crystals of full-length recombinant tetranectin (Nielsen *et al.*, 1996; Nielsen, 1996; Larsen *et al.*, 1996; Kastrup, 1996) has shown that the polypeptide encoded in exon 2 plus three residues encoded in exon 3 form a triple alpha helical coiled coil structure.

From the combination of sequence and structure data it becomes clear that trimerisation in tetranectin is in fact generated by a structural element (Fig. 2), comprising the amino acid residues encoded by exon two and the first three residues of exon 3 by an unusual heptad repeat sequence, that apparently is unique to tetranectin and other members of its group: This amino acid sequence (Fig. 2) is characterised by two copies of heptad repeats (abcdefg) with hydrophobic residues at a and d positions as are other alpha helical

coiled coils. These two heptad repeats are in sequence followed by an unusual third copy of the heptad repeat, where glutamine 44 and glutamine 47 not only substitute the hydrophobic residues at both the a and d position, but are directly involved in the formation of the triple alpha helical coiled coil structure. These heptad repeats are additionally flanked by two half-repeats with hydrophobic residues at the d and a position, respectively.

The presence of beta-branched hydrophobic residues at a or d positions in alpha helical coiled coil are known to influence the state of oligomerisation. In the tetranectin structural element only one conserved valine (number 37) is present. At sequence position 29 in tetranectin no particular aliphatic residue appears to be preferred.

In summary, it is apparent that the triple stranded coiled coil structure in tetranectin to a large extent is governed by interactions that are unexpected in relation to those characteristic among the group of known coiled coil proteins.

The TTSEs form surprisingly stable trimeric molecules (Examples 2, 3 and 4). The experimental observations, that **(1)** a substantial part of the recombinant proteins exists in the oligomeric state of - and can be cross-linked as - trimeric molecules even at 70°C and **(2)** that exchange of monomers between different trimers can only be detected after exposure to elevated temperature are evidence of a extremely high stability of the tetranectin trimerising structural element. This feature must be reflected in the amino acid sequence of the structural element. In particular, the presence and position of the glutamine containing repeat in the sequential array of heptad repeats is, together with the presence and relative position of the other conserved residues in the consensus sequence (Fig. 2), considered important for the formation of these stable trimeric molecules. For most practical uses the cysteine residue 50 should be mutagenized to serine, threonine, methionine or to any other amino

acid residue in order to avoid formation of an unwanted inter-chain disulphide bridge, which eventually would lead to uncontrolled multimerisation, aggregation and precipitation of a polypeptide product harbouring this sequence.

In particular in conjunction with the trimer-stabilising exon 1 encoded polypeptide (tetranectin residues 1 to 16, see Example 2), the tetranectin trimerising structural element is a truly autonomous polypeptide module retaining its structural integrity and propensity to generate a highly stable homotrimeric complex whether it is attached or not by a peptide bond at either or at both termini to other proteins. This unique property is demonstrated in the accompanying examples, which provide experimental proof, that polypeptide sequences derived from heterologous proteins may readily be trimerised when joined as fusion proteins to the tetranectin trimerising structural element. This remains valid irrespective of whether the heterologous polypeptide sequences are placed amino-terminally or carboxy-terminally to the trimerising element allowing for the formation of one molecular assembly containing up to six copies of one particular polypeptide sequence or functional entities, or the formation of one molecular assembly containing up to six different polypeptide sequences, each contributing their individual functional property.

Since three TTSEs of naturally occurring human tetranectin forms up a triple alpha helical coiled coil, it is preferred that the stable complex formed by the TTSEs of the invention also forms a triple alpha helical coiled coil.

The "tetranectin family" are polypeptides which share the consensus sequence shown in Fig. 2 or a sequence which are homologous at sequence level with this consensus sequence. Hence, monomer polypeptide constructs of the invention are preferred which comprise a polypeptide sequence which has at least 68% sequence identity with the consensus sequence shown in Fig. 2, but higher sequence identities are preferred, such

as at least 75%, at least 81%, at least 87%, and at least 92%.

By the term "heterologous moiety" is herein meant any chemical entity which can be linked covalently to a TTSE and to which the TTSE is not natively covalently bound. Hence, the heterologous moiety can be any covalent partner moiety known in the art for providing desired binding, detection, or effector properties. The heterologous moiety can be a ligand binding structure such as a receptor molecule or the ligand binding part of a receptor molecule, an antibody, an antigen binding antibody fragment, or a molecule having antibody characteristics such as e.g. the "diabodies" described in EP-A-0 672 142, or other ligand binding molecules such as avidin or streptavidin, or a lectin; a toxin such as ricin; a detectable label such as a fluorescence labelled molecule, a radioactively labelled molecule, an enzymatically labelled molecule; an *in situ* activatable substance, such as a molecule which can be induced by radiation to be radioactively or chemically active; an enzyme such as a peroxidase; a radioactive moiety such as a γ-, α-, β^--, or β^+-emitting molecule, e.g. a molecule comprising one or more radioactive isotopes selected from ^{14}C, ^{3}H, ^{32}P, ^{33}P, ^{25}S, ^{38}S, ^{36}Cl, ^{22}Na, ^{24}Na, ^{40}K, ^{42}K, ^{43}K, and any isotopes conventionally utilized for the purposes of facilitating detection of probes or the purposes of providing localized radiation so as to effect cell death; a cytokine such as an interferon or a leukotriene; a non-proteinaceous polymer such as a polymeric alkaloid, 11.a polyalcohol, a polysaccharide, a lipid and a polyamine; a photo cross-linking moiety, *i.e.* a chemical entity which effects cross-linking upon photo-activation; and a group facilitating conjugation of the monomer polypeptide construct to a target.

The heterologous moiety is preferably covalently linked to the TTSE by via a peptide bond to the N- or C-terminus of the TTSE peptide chain, via a peptide bond to a side chain in the TTSE or via a bond to a cysteine residue, but any way of

coupling covalently heterologous material to a polypeptide chain will be useful. The skilled person will know of such possibilities, e.g. by consulting the teachings of WO 95/31540 in this regard which are hereby incorporated by reference.

However, one interesting aspect of the invention relates to a monomer polypeptide construct of the invention comprising two heterologous moieties which are linked via peptide bonds to the N- and C-terminus, respectively. This approach introduces a number of possibilities in terms of e.g. linking larger entities with oligomers of the invention by having specific activities coupled to each end of the monomers (as explained in detail below, the oligomers of the invention may also utilise a version of this principle, where e.g. one N-terminus and one C-terminus of an oligomer are linked via peptide bonds to independent heterologous moieties).

In general, a complex between two or three monomers are described in the following way: three monomers having one TTSE each forms a trimer designated (1+1+1), whereas a dimer formed between a monomer with two TTSEs and a monomer with one TTSE is designated (1+2). Other (undesired) trimers can of course be formed, e.g. (2+2+1), where two TTSEs are not "in use", but it is preferred that the oligomers of the invention use all of their available TTSEs during complex formation. It should also be noted that the term "monomer polypeptide construct" is meant to designate a single polypeptide chain which may or may not have non-peptide groups coupled covalently to the polypeptide chain, whereas "dimeric polypeptide" or "dimer", "trimeric polypeptide" or "trimer" and "oligomer" (*i.e.* a dimer or trimer) in the present context are meant to designate non-covalent complexes of monomer polypeptide constructs. *I.e.*, the traditional definitions of monomers and multimers *do not* apply in the present specification and claims.

The TTSE as exemplified by exon 2 or exons 1 and 2 of human tetranectin, preferably so modified to allow only hetero-trimerisation between dissimilar (1+1+1) or (1+2) (cf. the below discussion) subunits may be deployed as a general affinity mediator, which can be coupled chemically to each member of a selection of target molecules. After such conjugation with TTSE the target molecules may be homo- or hetero-trimerised as desired for any application. Similar deployment of dimerisation, using as one partner a polypeptide harbouring two TTSE sequences in-line, separated by a linker sequence of suitable length and character, may bet yet more advantageous, as in such case absolute control of stoichiometry in complex formation would be possible. Thus, an important embodiment of the invention is a monomer polypeptide construct of the invention comprising 2 TTSEs which are covalently linked by a spacer moiety which allows both of the 2 TTSEs to take part in complex formation with a third TTSE not being part of the monomer polypeptide construct, but equally important is the embodiment of the invention where the monomer polypeptide construct comprises one single TTSE, so as to allow trimerisation between three monomers and hence providing the optimum degree of versatility with respect to the number of functional units which can be easily incorporated into one single complex.

In the embodiments where two TTSEs are present in the same monomer it is preferred that the spacer moiety has a length and a conformation which favours complex formation involving both of the two TTSEs which are covalently linked by the spacer moiety. In this way, problems arising from undesired formation of trimers of the formats (2+1+1), (2+2+2), and (2+2+1) (wherein only one TTSE of each monomer participates in complex formation) can be diminished. Design and preparation of suitable spacer moieties are known in the art and are conveniently effected by preparing fusion polypeptides having the format $TTSE^1$-Spacer-$TTSE^2$, where the spacer moiety is a polypeptide fragment (often a relatively inert one), so as to

avoid undesired reactions between the spacer and the surroundings or the TTSEs.

One typical scenario, where such modification may be advantageous is the case of immunological detection where a chemical conjugate of an antibody with enzymes such as peroxidase is used for in situ staining purposes in tissue or on western blots.

A similar, but yet different, application example would be the deployment of TTSE to mediate conjugation of e.g. alkaline phosphatase and an oligonucleotide which would allow in situ identification of a given mRNA in a tissue sample concurrently with idenfification of any other mRNA molecule e.g. by interconnection of a second appropriate oligonucleotide and a signalling/visualisation molecule using e.g. the biotin - avidin/streptavidin affinity pair for conjugation. The point of having two or more selective affinity systems available for conjugating oligonucleotide probes and detector molecules is that as many different sequences may be detected simultaneously as there are affinity sets available.

In terms of chemistry required to exploit TTSE as a conjugating affinity-contributing agent, the peptide corresponding to exon 2 will have a sufficient affinity for most purposes, but incorporation of all, or some segment of the exon 1 polypeptide will serve to increase affinity and stability. The properties of tetranectin mutants in which many of hydrophilic (e.g. lys and glu) residues that are largely exterior in the coiled coil structure have been replaced with alanine appear similar to the native protein, suggesting that is indeed possible without interfering very much with stability of the trimeric structure to replace all glu, asp and lys residues by a combination of gln, asn, arg or ala, and thereby generate a sequence that, as an N-terminally blocked synthetic peptide, would be very easy to convert into a chemically stable active-ester component, e.g. an N-hydroxy succinimide ester of an acetylated peptide, that could react

with (and thereby couple to) any exposed lysine side chain in a target molecule of interest. Such peptide synthesis, activation and coupling chemistry will be readily designed and applied by a person skilled in the art of peptide chemistry, as will indeed any other conjugation chemistry, like the attachment and use of photo-activatable moieties like e.g. phenyl azides.

In conclusion, it seems that the most important structure in native TTSE is the consensus sequence shown in Fig. 2, and that large variations in the polypeptide chain may be allowed. Hence, one advantageous embodiment of the monomer polypeptide construct of the invention is one where at least one amino acid residue selected from the group consisting of amino acid residue nos. 6, 21, 22, 24, 25, 27, 28, 31, 32, 35, 39, 41, 42, is/are substituted by any non-helix breaking amino acid residue, the amino acid residue numbering referring to amino acid residues in SEQ ID NO: 7. All these residues have been shown not to be directly involved in the intermolecular interactions which stabilises the trimeric complex between three TTSEs of native tetranectin monomers and it is therefore expected that these amino acids may be safely substituted with any amino acid which will not have an adverse effect on helix formation (notably proline, which introduces a rigid bend in a polypeptide chain).

Another advantageous embodiment of the monomer polypeptide construct of the invention is one which is free from any free amino and/or carboxy groups. This would favour synthesis of a TTSE by means of solid or liquid phase peptide synthesis, since there would be no need of introducing any protective groups during peptide synthesis.

Since the consensus sequence of Fig. 2 is believed important and since this consensus sequence embraces the above-discussed heptad repeat, it is according to the invention preferred that the TTSE comprises a repeated heptad having the formula a-b-c-d-e-f-g (N to C), wherein residues a and d

generally are hydrophobic amino acids. However, since "a" and "d" in the third of the complete heptads of all known members of the tetranectin family are constituted of glutamine, it is most preferred that the TTSE comprises the heptad repeated 3 times and that the last occurrence of the heptad has a glutamine residue corresponding to residues a and d.

Since exon 2 of native members of the tetranectin family seems to contain the necessary elements to effect stable trimerisation, it is preferred that the monomer polypeptide construct is free of substantial parts of tetranectin which is encoded by exon 3 and/or lacks substantial parts of tetranectin which is encoded by exon 1. However, since exon 1 encoded material seems to stabilise the trimeric native tetranectin, it is especially preferred that all or part of exon 1 is part of the monomer polypeptide construct, and it also seems to be rational to include the first three amino acids encoded by exon 3, since these are known to take part of the formation of the native triple alpha helical coiled coil in human tetranectin.

One particularly interesting embodiment of the invention is the possibility of designing oriented molecular assemblies, where one or more functional entities are located N-terminally to the trimerising element and one or more functional entities are located C-terminally to the element. Such types of design may be particularly advantageous where a certain relative ratio is desired among the different functional entities included in a specific molecular unit. Such type of design may in addition be used if one or more functional entities for either structural or functional reasons appear incompatible within the same construct. Such may be the case if one or more of the functional entities are expressed by large or bulky protein domains which for steric reasons might prevent formation of the trimeric molecular unit due to sterical constraints.

The possibility of constructing bi-polar three-way fusion proteins in which one functionality is placed N-terminally to the coiled coil structure and a different functionality is placed C-terminally is additionally advantageous in applications where large spatial separation between the two functionalities are desirable for optimal function. Examples of such application are e.g. the deployment of binding domains (e.g. antibody-derived binding modules) for recognition and binding to binding sites located at or close to large structures like cell membranes in cases where it is advantageous to allow for binding of the other end of the trimerised molecule to a different, but also bulky target.

Hence, as discussed above, the oligomers of the invention may be used to join e.g. bulky surfaces by the oligomer according to the invention comprising at least one heterologous moiety which is positioned N-terminally to a TTSE and at least one heterologous moiety which is positioned C-terminally to a TTSE. The two heterologous moieties can be either part of the same monomer polypeptide construct or parts of two separate monomer polypeptide constructs.

The extraordinarily high stability of any trimer containing the tetranectin trimerisation module under physiological buffer and temperature condition (i.e. absence of denaturant, temperature not exceeding 40°C) in combination with the ease by which exchange of monomer subunits between trimers can be effected by incubation at moderately elevated temperature or in the presence of denaturants provide for a unique opportunity to deploy the trimerisation module as a vehicle to allow the construction of "pick-and-mix" conjugates prepared from previously fabricated collections of homotrimeric molecules. To illustrate the versatility of this design opportunity by way of theoretical example, let us assume that (1) a collection of twenty different antibody constructs (e.g. in the format of single-chain Fv) each of its own characteristic binding specificity, has been selected and then turned into homo-trimeric molecules by fusion to a tetranectin trimerisa-

tion module, and let us also assume that a set of twenty different effector molecules (e.g. toxin domains) have similarly been prepared and also conjugated to the tetranectin trimerisation module. A user provided with prefabricated collections of twenty different antibody constructs and twenty different toxin constructs - 40 different reagents in all - has the opportunity then to prepare 400 different toxin-antibody conjugates, simply by mixing a first preferred component from one reagent collection with a second preferred reagent from the other collection and then subject this binary mixture to conditions, i.e. gentle heating or incubation with a suitable level of denaturant, to accomplish subunit exchange among all trimeric molecular species in the mixture. After the subunit exchange step the desired heterobifunctional reagent will be present in the mixture as a major component of the mixture and may then be deployed as such to accomplish a given purpose or, alternatively apply a simple purification step to isolate his favoured heterofunctional binary reagent from any remaining mono-functional trimer species by a simple standard protein purification step, easily designed using standard techniques known in the field of protein purification.

A further enhancement of the versatility of the "pick-and-mix" technology may be achieved by including a specific affinity purification tag on each array of trimerisation module - probe/effector/indicator conjugate, fused directly in-line or, alternatively, fused via a cleavable linker (a polypeptide segment containing e.g. a factor X_a or an enterokinase recognition/cleavage site) to the affinity tag. More specifically, if each of three libraries were tagged with affinity handles a, b and c, respectively, that were recognised by binding substances A, B and C, respectively, pure heterotrimers, composed of one member of each library, could be obtained in a three-step affinity purification procedure designed to allow selective recovery of only such trimers that exhibit affinity for substances A and B and C. If, for any reason, subsequent removal of the affinity tags

were desirable, and the constructs had been prepared to include cleavable linkers, isolation of the pure heterotrimer, liberated from all affinity tags, could be accomplished by three further affinity purification steps, arranged to isolate only material that would bind to neither substance A nor substance B nor substance C.

Obviously, the scope of "pick-and-mix" design of user-preparable heterofunctional complexes apply not only to the formation of binary hetero-functionality, but would apply by logic extension to the formation of ternary hetero-functionality: To envisage the wealth of possibilities that are inherent to the concept of ternary hetero-functionality in a further theoretical example along the lines given above, three sets of reagent collections, each comprising 20 different functional characteristics, i.e. a collection of in toto 60 different homotrimers would allow "pick-and-mix" preparation of 8,000 different tri-functional molecules.

The basic tetranectin trimerisation module will, essentially indiscriminately, form homo- and hetero-trimers with any molecule that also contains a trimerisation module. For some applications it may be advantageous to have available specially engineered derivatives of the tetranectin trimerisation module, which have been reengineered to disallow homotrimer formation and hence only allow hetero-trimerisation. Thus, an important embodiment of the monomer polypeptide construct of the invention is constructed/reengineered so as to disfavour formation of complexes between identical TTSEs; this also has the implication that oligomers of the invention can advantageously be comprised of monomer polypeptide constructs which are designed so as to disfavour formation of trimers including two monomer polypeptide constructs having identical TTSEs.

The design/reengineering may be accomplished by introduction of amino acid substitution at sites in the polypeptide intimately involved in the formation and stability of the trimer

and, simultaneously, in a different construct introduce a compensatory amino acid substitution, all in all removing symmetry between individual monomer components of the triple helical structure so that the structural complementarity profile only allows the formation of hetero-trimers, but is incompatible with some or each of the homotrimer species.

A yet different way to deploy the tetranectin trimerisation module as a vehicle to accomplish rational formation of bifunctionalisation would require the interconnection of the C-terminus of one monomer to the N-terminus of a second monomer in the triple-helical structure. The basic requirement for such an intervening polypeptide is, that allowed spatial distances between its N- and C-termini must be compatible with the spacing inherent to the structural requirements given by the architecture of the tetranectin trimerisation module. The construction of an intervening connecting polypeptide allowed according to such criteria would be readily accomplished by an average person skilled in the art of protein engineering, as an ample collection of examples of the deployment of, usually flexible, spacer sequences are known both in nature and in designed proteins. Due to the expected entropic contribution to interaction energy in a molecule in which two of the three tetranectin trimerisation module components are covalently tied together, such a molecule would show great preference for selecting any molecule containing only a single copy of the tetranectin trimerisation module component, as this selection would be energetically favoured. Hence, conjugation of one functional protein component to a suitably selected covalently dimerised tetranectin trimerisation module component and conjugation of a different functional protein component to a single-copy element of the trimerisation sequence would provide for the preferential formation of a 1:1 bifunctional complex and suppression of formation of any other complex.

The monomers of the invention may be prepared by methods generally known in the art, using exclusively or in combina-

tion the techniques of recombinant protein production, peptide synthesis (liquid phase or solid phase), and traditional chemical coupling of heterologous moieties to a peptide chain or to specific residues therein. Hence the invention also relates to a method of preparing the monomer polypeptide construct of the invention, the method comprising

- isolating the monomer polypeptide construct from a culture comprising a host cell which carries and expresses a nucleic acid fragment which encodes the monomer polypeptide construct,

- synthesizing, by means of chemical peptide synthesis, the monomer polypeptide construct and subsequently isolating the monomer polypeptide construct from the reaction mixture,

- preparing a TTSE in a culture comprising a host cell which carries and expresses a nucleic acid fragment which encodes the TTSE, subsequently linking covalently at least one heterologous moiety to the TTSE, and thereafter isolating the resulting monomer polypeptide construct, or

- synthesizing, by means of chemical peptide synthesis, a TTSE, subsequently linking covalently at least one heterologous moiety to the TTSE, and thereafter the isolating the resulting monomer polypeptide construct from the reaction mixture,

and optionally subjecting the monomer polypeptide construct to further processing.

The nucleic acid fragment which is mentioned above is also a part of the invention and is defined as a nucleic acid fragment in isolated form which encodes a TTSE as defined herein or which encodes the polypeptide part of a monomer polypeptide construct according to the invention, with the proviso that the nucleic acid fragment is different from one

that encodes native members of the tetranectin family, and that the nucleic acid fragment is different from one that encodes any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23, the sequences of which are shown in SEQ ID NOs: 24-27.

The above mentioned host cell (which is also a part of the invention) can be prepared by traditional genetic engineering techniques which comprises inserting a nucleic acid fragment (normally a DNA fragment) encoding the polypeptide part of a monomer polypeptide construct of the invention into a suitable expression vector, transforming a suitable host cell with the vector, and culturing the host cell under conditions allowing expression of the polypeptide part of the monomer polypeptide construct. The nucleic acid fragment encoding the polypeptide may be placed under the control of a suitable promoter which may be inducible or a constitutive promoter. Depending on the expression system, the polypeptide may be recovered from the extracellular phase, the periplasm or from the cytoplasm of the host cell.

Suitable vector systems and host cells are well-known in the art as evidenced by the vast amount of literature and materials available to the skilled person. Since the present invention also relates to the use of the nucleic acid fragments of the invention in the construction of vectors and in host cells, the following provides a general discussion relating to such use and the particular considerations in practising this aspect of the invention.

In general, of course, prokaryotes are preferred for the initial cloning of nucleic sequences of the invention and constructing the vectors useful in the invention. For example, in addition to the particular strains mentioned in the more specific disclosure below, one may mention by way of example, strains such as *E. coli* K12 strain 294 (ATCC No. 31446), *E. coli* B, and *E. coli* X 1776 (ATCC No. 31537). These

examples are, of course, intended to be illustrative rather than limiting.

Prokaryotes are also preferred for expression, since efficient purification and protein refolding strategies are available. The aforementioned strains, as well as *E. coli* W3110 (F-, lambda-, prototrophic, ATCC No. 273325), bacilli such as *Bacillus subtilis*, or other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcesans*, and various *Pseudomonas* species may be used.

In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species (see, e.g., Bolivar et al., 1977). The pBR322 plasmid contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR plasmid, or other microbial plasmid or phage must also contain, or be modified to contain, promoters which can be used by the microorganism for expression.

Those promoters most commonly used in recombinant DNA construction include the B-lactamase (penicillinase) and lactose promoter systems (Chang et al., 1978; Itakura et al., 1977; Goeddel et al., 1979) and a tryptophan (trp) promoter system (Goeddel et al., 1979; EPO Appl. Publ. No. 0036776). While these are the most commonly used, other microbial promoters have been discovered and utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally with plasmid vectors (Siebwenlist et al., 1980). Certain genes from prokaryotes may be expressed efficiently in *E. coli* from their own promoter sequences, precluding the need for addition of another promoter by artificial means.

In addition to prokaryotes, eukaryotic microbes, such as yeast cultures may also be used. *Saccharomyces cerevisiase*, or common baker's yeast is the most commonly used among eukaryotic microorganisms, although a number of other strains are commonly available. For expression in *Saccharomyces*, the plasmid YRp7, for example, is commonly used (Stinchcomb et al., 1979; Kingsman et al., 1979; Tschemper et al., 1980). This plasmid already contains the trpl gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan for example ATCC No. 44076 or PEP4-1 (Jones, 1977). The presence of the trpl lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan.

Suitable promoting sequences in yeast vectors include the promoters for 3-phosphoglycerate kinase (Hitzman et al., 1980) or other glycolytic enzymes (Hess et al., 1968; Holland et al., 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. In constructing suitable expression plasmids, the termination sequences associated with these genes are also ligated into the expression vector 3' of the sequence desired to be expressed to provide polyadenylation of the mRNA and termination.

Other promoters, which have the additional advantage of transcription controlled by growth conditions are the promoter region for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, and the aforementioned glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Any plasmid vector containing a yeast-compatible promoter, origin of replication and termination sequences is suitable.

In addition to microorganisms, cultures of cells derived from multicellular organisms may also be used as hosts. In principle, any such cell culture is workable, whether from vertebrate or invertebrate culture. However, interest has been greatest in vertebrate cells, and propagation of vertebrate in culture (tissue culture) has become a routine procedure in recent years (Tissue Culture, 1973). Examples of such useful host cell lines are VERO and HeLa cells, Chinese hamster ovary (CHO) cell lines, and W138, BHK, COS-7 293 and MDCK cell lines.

Expression vectors for such cells ordinarily include (if necessary) an origin of replication, a promoter located in front of the gene to be expressed, along with any necessary ribosome binding sites, RNA splice sites, polyadenylation site, and transcriptional terminator sequences.

For use in mammalian cells, the control functions on the expression vectors are often provided by viral material. For example, commonly used promoters are derived from polyoma, Adenovirus 2, and most frequently Simian Virus 40 (SV40). The early and late promoters of SV40 virus are particularly useful because both are obtained easily from the virus as a fragment which also contains the SV40 viral origin of replication (Fiers et al., 1978). Smaller or larger SV40 fragments may also be used, provided there is included the approximately 250 bp sequence extending from the *Hind*III site toward the BglI site located in the viral origin of replication. Further, it is also possible, and often desirable, to utilize promoter or control sequences normally associated with the desired gene sequence, provided such control sequences are compatible with the host cell systems.

An origin of replication may be provided either by construction of the vector to include an exogenous origin, such as may be derived from SV40 or other viral (e.g., Polyoma, Adeno, VSV, BPV) or may be provided by the host cell chromosomal replication mechanism. If the vector is inte-

grated into the host cell chromosome, the latter is often sufficient.

Upon production of the polypeptide monomer constructs it may be necessary to process the polypeptides further, e.g. by introducing non-proteinaceous functions in the polypeptide, by subjecting the material to suitable refolding conditions (e.g. by using the generally applicable strategies suggested in WO 94/18227), or by cleaving off undesired peptide moieties of the monomer (e.g. expression enhancing peptide fragments which are undesired in the end product).

In the light of the above discussion, the methods for recombinantly producing the monomer polypeptide construct of the invention are also a part of the invention, as are the vectors carrying and/or being capable of replicating the nucleic acids according to the invention in a host cell or a cell-line. According to the invention the expression vector can be e.g. a plasmid, a cosmid, a minichromosome, or a phage. Especially interesting are vectors which are integrated in the host cell/cell line genome after introduction in the host.

Another part of the invention are transformed cells (useful in the above-described methods) carrying and capable of replicating the nucleic acid fragments of the invention; the host cell can be a microorganism such as a bacterium, a yeast, or a protozoan, or a cell derived from a multicellular organism such as a fungus, an insect cell, a plant cell, or a mammalian cell. Especially interesting are cells from the bacterial species *Escherichia*, *Bacillus* and *Salmonella*, and a preferred bacterium is *E. coli*.

Yet another part of the invention relates to a stable cell line producing the polypeptide part of a monomer polypeptide construct according to the invention, and preferably the cell line carries and expresses a nucleic acid of the invention.

On the basis of the above discussions it will be clear to the skilled person that also the oligomers resulting from the complex formation between the monomer constructs of the invention are important parts of the invention. Hence the invention also pertains to an oligomer which is comprised of two monomer polypeptide constructs according to the invention which comprises at least three TTSEs, or which is comprised of three monomer polypeptide constructs according to the invention which each only contain one single TTSE.

As is explained herein and shown in the examples, the oligomers of the invention are stable at temperatures up to 70°C and it is therefore especially preferred that the oligomers of the invention are stable at temperatures above physiological ones, e.g. that the oligomers are stable in the temperature range 50-70°C.

Also a part of the invention is a method for preparing a dimeric oligomer of the invention which comprises

- admixing a monomer polypeptide construct which includes two TTSEs (construct 1) with a monomer polypeptide construct which includes only one TTSE (construct 2),

- effecting the two TTSE's of construct 1 to complex with the TTSE of construct 2 (this can be done by thermal treatment, *i.e.* heating to a temperature which ensures denaturation followed by subsequent cooling allowing renaturation, or this can be done by denaturing/renaturing effected by changes in the chemical environment), and

- isolating the resulting dimer and optionally subjecting the dimer to further processing (cf. the above discussion of further processing, but it should also be mentioned that the further processing could include non-covalent coupling of interesting and relevant moieties to the dimeric oligomer).

Consequently, the method for producing a trimeric oligomer is also a part of the invention and comprises the steps of

- admixing three monomer polypeptide constructs of the invention with each other,

- effecting complex formation between one TTSE of each monomer polypeptide construct, and

- isolating the resulting trimer and optionally subjecting the trimeric oligomer to further processing.

The considerations applying to complex formation and further processing mentioned above apply to this method also.

Finally, in view of the detailed discussion above of the "pick-and-mix" aspect of the invention, the invention also pertains to a kit comprising

- a first package comprising at least one container means, each at least one container means containing a monomer polypeptide construct of the invention,

- a second package comprising at least one container means, each at least one container means in the second package containing a monomer polypeptide construct of the invention, the second package being different from the first package with respect to choice and/or number of monomer polypeptide constructs included therein, and optionally

- a third package comprising at least one container means, each at least one container means in the third package containing a monomer polypeptide construct of the invention, the second package being different from the first and second packages with respect to choice and/or number of monomer polypeptide constructs included therein.

It is preferred that the at least one container means in each package contains mutually distinct monomer polypeptide constructs, and it is especially preferred that all container means comprised in the kit comprises mutually distinct polypeptide constructs.

EXAMPLE 1

Design and construction of the pTH6trip E. coli expression vectors for the production of trimerised chimeric fusion proteins.

The plasmid clone pT7H6FXTN123 (Example 2) was used as template for amplification in two Polymerase Chain Reactions (PCR) (Saiki *et al.*, 1988) with the primer pairs trip-N (SEQ ID NO: 1) and trip-Ca (SEQ ID NO: 2) and trip-N (SEQ ID NO: 1) and trip-Cb (SEQ ID NO: 3), respectively. The amplified DNA fragments, tripa, comprising nucleotide sequences encoding an IQGR cleavage site for the restriction protease FX_a (SEQ ID NO: 4) followed by two sites for the restriction nucleases BglII and KpnI, the nucleotide sequence encoding the tetranectin polypeptide sequence for Glu 1 to Lys 52 (SEQ ID NO: 5) followed by recognition sites for the three restriction endonucleases BamHI, HindIII, and EcoRI, respectively, and tripb, comprising nucleotide sequences encoding an IQGR cleavage site for the restriction protease FX_a (SEQ ID NO: 4) followed by two sites for the restriction nucleases BglII and KpnI, the nucleotide sequence encoding the tetranectin polypeptide sequence for Glu 1 to Val 49 (SEQ ID NO: 6) followed by recognition sites for the three restriction endonucleases BamHI, HindIII, and EcoRI, respectively, were subcloned into the plasmid pT7H6 (Christensen *et al.*, 1991), yielding pTtripa and pTtripb, respectively (Figs. 3 and 4).

EXAMPLE 2

Tetranectin, localisation of the trimerising structural element and stability of the triple alpha helical coiled coil.

The cDNA encoding the reading frame corresponding to the mature tetranectin single chain (SEQ ID NO: 7) was cloned by specific amplification in a Polymerase Chain Reaction (PCR) (Saiki *et al.*, 1988) of the nucleotide sequences from amino acid residue Glu1 to Val181 using 1st strand oligo-dT primed cDNA synthesized from total human placental RNA as template. Primers used in the PCR were SEQ ID NO: 8 and SEQ ID NO: 9. RNA extraction and cDNA synthesis were performed using standard procedures. The amplified reading frame encoding the monomer subunit of tetranectin was at the 5'-end, via the PCR-reaction, linked to nucleotide sequences encoding the amino acid sequence SEQ ID NO: 10 which constitute an IEGR cleavage site for the bovine restriction protease FX_a (Nagai, and Thøgersen, 1987). A glycine residue was, due to the specific design of the 5'-PCR primer (SEQ. ID NO. 8), inserted between the C-terminal arginine residue of the FX_a cleavage site (SEQ ID NO. 10) and the tetranectin Glu1-residue. The amplified DNA fragment was subcloned into the *E. coli* expression vector pT_7H_6 (Christensen *et al.*, 1991) producing the plasmid pT_7H_6FX-TN123 expressing the tetranectin monomer H6FXTN123 (SEQ ID NO: 25) and into pT_7CIIH_6, which is a derivative of pT_7H_6, where the amino-terminal 32 amino acid residues of the lambda CII protein (SEQ ID NO. 11) are inserted 5' of the six histidine residues (SEQ ID NO. 12) as outlined in Fig. 5, yielding pT_7CIIH_6FX-TN123 expressing the tetranectin fusion protein CIIH6FXTN123 (SEQ ID NO: 24). The amino acid sequence of the expressed proteins are shown in Fig. 6 (in SEQ ID NO: 7 is given the amino acid sequence of the mature tetranectin protein). Furthermore three additional derivatives of tetranectin were constructed (Fig. 8): H6FXTN12 comprising the tetranectin amino acid residues Glu1 to Val49 (SEQ ID NO: 6), H6FXTN23 comprising the tetranectin

amino acid residues Val17 to Val181 (SEQ ID NO: 7), and H6FXTN3 (SEQ ID NO: 30) comprising the tetranectin amino acid residues Ala45 to Val181 (SEQ ID NO: 7). These three tetranectin derivatives were constructed by specific amplification in a PCR using pT_7H_6FX-TN123 as template and the primer-pairs SEQ ID NO: 8 and SEQ ID NO: 13, SEQ ID NO: 14 and SEQ ID NO: 9, and SEQ ID NO: 15 and SEQ ID NO: 9, respectively. The amplified DNA fragments were subcloned into the *E. coli* expression vector pT_7H_6 producing the plasmids pT_7H_6FX-TN12, pT_7H_6FX-TN23, and pT_7H_6FX-TN3, respectively (Fig. 7).

To prepare recombinant tetranectin and its derivatives, each of the plasmids pT_7H_6FX-TN123, pT_7CIIH_6FX-TN123, pT_7H_6FX-TN12, pT_7H_6FX-TN23, and pT_7H_6FX-TN3 were grown in medium scale (4 x 1 litre; 2xTY medium, 5 mM $MgSO_4$ and 100 μg ampicillin) in *E. coli* BL21 cells, as described by Studier *et al.* (1990). Exponentially growing cultures at 37°C were at OD_{600} 0.8 infected with bacteriophage lambda CE6 at a multiplicity of approximately 5. Cultures were grown at 37°C for another three hours and the cells harvested by centrifugation.

Cells were resuspended in 150 ml of 0.5 M NaCl, 10 mM Tris-HCl pH 8, and 1 mM EDTA pH 8. Phenol (100 ml adjusted to pH 8) was added and the mixture sonicated to extract the total protein. Protein was precipitated from the phenol phase by 2.5 volumes of ethanol and centrifugation.

The protein pellet was dissolved in a buffer containing 6M guanidinium chloride, 50 mM Tris-HCl pH 8 and 0.1 M dithioerythriol. Following gel filtration on Sephadex G-25 (Pharmacia, Sweden) into 8 M Urea, 1 M NaCl, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol, the crude protein preparation was applied to a Ni^{2+} activated NTA-agarose column (Ni^{2+}NTA-agarose, 75 ml pre-washed with 8 M urea, 1 M NaCl, 50 mM Tris-HCl pH 8, and 10 mM 2-mercaptoethanol) for purification (Hochuli *et al.*, 1988) and refolding of the fusion proteins, H6FXTN123, CIIH6FXTN123, H6FXTN12, H6FXTN23, and H6FXTN3.

For this study we chose to prepare our own Ni^{2+}NTA-agarose matrix. A carbodiimide coupling of the N-(5-amino-1-carboxy-pentyl) iminodiacetic acid metal ligand (synthesis route as described by Döbeli & Hochuli (EP-A-0 253 303)) to a rigid agarose matrix (Sepharose CL-6B, Pharmacia, Sweden) was performed:

8 g of N-(5-amino-1-carboxypentyl)iminodiacetic acid from the synthesis procedure in 50 ml was adjusted to pH 10 by addition of 29 g of $Na_2CO_3(10\ H_2O)$ and added to a stirred suspension of activated Sepharose CL-6B in 1 M Na_2CO_3. Reaction was allowed overnight. The Sepharose CL-6B (initially 100 ml suspension) was activated after removal of water by acetone with 7 g of 1,1'-carbonyldiimidazol under stirring for 15 to 30 min. Upon activation the Sepharose CL-6B was washed with acetone followed by water and 1 M Na_2CO_3.

The NTA-agarose matrix was loaded into a column and "charged" with Ni^{2+} by slowly passing through 5 column volumes of a 10% $NiSO_4$ solution. The amount of Ni^{2+} on the NTA-agarose matrix, prepared by this procedure, has been determined to 14 µmol per ml matrix. After charging the Ni^{2+}NTA-agarose column was washed with two column volumes of water, one column volume of 1 M Tris-HCl pH 8 and two column volumes of loading buffer before stirred mixing of the Ni^{2+}NTA-agarose matrix with the crude protein extracts in a breaker for 15 to 30 min. All buffers prepared for liquid chromatography were degassed under vacuum prior to addition of reductant and/or use.

The Ni^{2+}NTA-agarose matrix - crude extract mixture was packed in standard glass columns for liquid chromatography (internal diameter: 2.6 cm) to a volume of approximately 40 ml. The columns were washed with 200 ml of 8 M urea, 1 M NaCl, 50 mM Tris-HCl pH 8, and 10 mM 2-mercaptoethanol (Buffer I) and 100 ml 6 M guanidinium chloride, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol (Buffer II) and the adsorbed tetranectin derived fusion proteins H6FXTN123, H6CIIFXTN123, H6FXTN23,

and H6FXTN3 refolded using the cyclic refolding procedure as described (Thøgersen *et al.*, WO 94/18227).

The fusion protein H6FXTN12 was refolded by removing the guanidinium chloride and 2-mercaptoethanol of buffer II in a gradient over 5 column volumes into 50 mM Tris-HCl pH 8 and 0.5 M NaCl. After completion of the refolding procedures the tetranectin derived fusion proteins were eluted from the Ni^{2+}NTA-agarose columns with a buffer containing 0.5 M NaCl, 50 mM Tris-HCl, 25 mM EDTA pH 8. The tetranectin fusion proteins H6FXTN123, H6FXTN23, and H6FXTN3 were cleaved with FX_a at 4°C overnight in a molar ratio of 1:300. After FX_a cleavage the protein samples were concentrated 10 fold by ultrafiltration on YM10 membranes (Amicon). After ten times dilution of the protein sample with 2 mM $CaCl_2$, the recombinant tetranectin derivatives TN123, TN23, and TN3 were isolated by ion-exchange chromatography on Q-Sepharose (Pharmacia, Sweden) in a linear gradient over 10 column volumes from 10 mM Tris-HCl pH 8, 2 mM $CaCl_2$ to 10 mM Tris-HCl pH 8, 2 mM $CaCl_2$, and 0.5 M NaCl. After elution from the Ni^{2+}NTA-agarose columns the fusion proteins H6CIIFXTN123 and H6FXTN12 were likewise concentrated 10 fold by ultrafiltration on YM10 membranes and gelfiltrated into buffer containing 25 mM Tris-HCl pH 8, 25 mM NaCl, and 2 mM $CaCl_2$, before purification of correctly folded monomer by ion-exchange chromatography on Q-Sepharose as described.

Recombinant full length tetranectin (TN123) produced by these procedures have been analyzed with respect to binding to plasminogen kringle 4 and immobilised fucoidan, expression of antigenic sites, and localization of disulphide bridges. In all criteria tested the produced TN123 behaved identically to isolated naturally human tetranectin (data not shown). Furthermore TN123 and TN3 have been crystallized (Kastrup *et al.*,1996) and the structure has also been determined, all of which bear evidence that a single unique and biologically active folded product had indeed been produced.

Analytical gelfiltration analysis of rTN proteins.

Analytical gelfiltration of the recombinant tetranectin derivatives TN123, TN3, and TN23 (Fig. 9) were performed on a Superose 12 HR 10/30 column (Pharmacia, Sweden) with a total volume of 25 ml in 100 mM NaCl and 50 mM Tris-HCl pH 8 and a flow rate of 0.2 ml/min. The K_{av} value is defined by, $K_{av}=(Ve-Vo)/(Vc-Vo)$.

The gelfiltration analysis of TN123 and TN23 show that both proteins are exclusively found as trimers in solution (K_{av} values of 0.27 and 0.29, respectively), whereas TN3 appeared monomeric (K_{av}:0.41).

Chemical cross-linking of tetranectin and derivatives

The recombinant tetranectin derivatives TN123, TN3, and TN23, together with the fusion proteins CIIH6FXTN123 and H6FXTN12 or mixtures of these derivatives at 1 mg/ml concentrations in cross-linking buffer (0.1 M Sodium borate, pH 9.1) were incubated with dimethylsuberimidate (DMSI, Sigma). 10 µl aliquots of protein solution were incubated with 1 µl aliquots of DMSI stock solution (20 mg/ml in cross-linking buffer) for 30 minutes at 25°C before addition of 2 µl quenching buffer (3 M Tris-HCl, pH 9). Subunit exchange between preformed homo-oligomers was induced by subjecting protein mixtures to heat shock treatment. Five µl aliquots of each protein solution (1 mg/ml stocks) were mixed at 0°C in standard polypropylene microcentrifuge tubes, transferred to a water bath at 70°C for the time spans indicated, and then further incubated for 15 minutes at 25°C before reaction with DMSI.

Prior to analysis by SDS-PAGE (12% gels) of the cross-linked products the reaction samples were boiled in the presence of SDS and mercaptoethanol.

Cross-linking analysis of TN123 and the fusion protein CIIH6FXTN123 showed that no detectable subunit exchange between pre-formed homo-oligomers in a mixture of TN123 and CIIH6FXTN123 was found after 16 hours at room temperature (Fig. 10). Subunit exchange could be induced by incubating the protein mixture at 70°C for 15 seconds or longer before cooling to room temperature and addition of DMSI. SDS-PAGE analysis showed the presence of four trimer bands above 95 kDa (corresponding to two homo-trimers and two hetero-trimers) and three dimer bands (corresponding to two homo-dimers and one hetero-dimer) in the gel between 43 and 55 kDa, in a relative abundance in agreement with random association of monomer subunits into trimers after subunit exchange. It should be noted, that molecular weight markers have only been included on the SDS-PAGE gels for crude calibration and orientation of the gels.

The trimeric organization of tetranectin was further corroborated by cross-linking studies of the proteins H6FXTN12, TN23, and TN3 and mixtures between them (Fig. 11). The tetranectin derivative TN3, containing only the CRD, could not be cross-linked even at high protein concentrations and did not interfere with the cross-linking of rTN123. Likewise, the derivative TN23, containing exon 2 and the CRD, appeared monomeric after cross-linking and was found not to interfere with trimerisation of TN123 during subunit exchange. Dimeric TN23 molecules found at low abundance in the sample probably reflects contaminating misfolded disulphide bridged dimers. The fusion protein H6FXTN12 formed homo-trimers upon cross-linking and generated hetero-trimers with TN123 after subunit exchange. Because of the difference in size of full length tetranectin (TN123) and H6FXTN12 the possible nine protein bands resulting from chemical cross-linking are: The four trimers [$(TN123)_3$, $(TN123)_2(H6FXTN12)$, $(TN123)(H6FXTN12)_2$, and $(H6FXTN12)_3$] at approx. 95 kDa , 50 kDa, 37 kDa, and 20 kDa, respectively; the three dimers [$(TN123)_2$, $(TN123)(H6FXTN12)$, and $(H6FXTN12)_2$] at approx. 45 kDa, 30

kDa, and 15 kDa, respectively; and the two monomers TN123 at 23 kDa and H6FXTN12 at 9 kDa.

Taken together, the gel filtration and the cross-linking analysis of the tetranectin derivatives show that tetranectin, like the collectin group of C-type lectins, is a trimeric molecule and that amino acid residues directly shown to be involved in trimerisation of the tetranectin monomer are located in exon 2 of the protein (Val17 - Val49). Furthermore subunit exchange between the trimeric molecules could only be observed after heat denaturation. Amino acid residues Glu1 to Asp16 of tetranectin are critical to chemical cross-linking with DMSI and more important appear to stabilize the trimeric molecule because the cross-linking analysis of the mixture TN123 and TN23 showed no decrease in TN123 formation after heat denaturation and possible subunit exchange (Fig. 11). The stability of the tetranectin trimer was corroborated by a cross-linking analysis with DMSI at different temperatures. Fifteen µl TN123 at 0.3 mg/ml concentration was pre-incubated 10 min. at either 37°C, 50°C, 60°C, or 70°C before addition of 2 µl DMSI (20 mg/ml). The reaction was allowed to proceed for 15 min. before reaction was quenched with 5 µl of 3M Tris-HCl pH 9.1 and the reaction mixtures allowed to cool to room temperature. SDS-PAGE analysis of reduced samples (Fig. 12) showed, that trimers are readily detectable even at 60°C, although a competing pattern of cross-linking specimens increases at increasing temperatures. The appearance of other cross-linking specimens is probably due to the unfolding of the CRD. The stability of the tetranectin trimerising structural element is further analyzed using a designed chimeric protein in Example 3.

EXAMPLE 3

Design and construction of the recombinant chimeric protein TRIPB-UB - the tetranectin trimerising structural element and ubiquitin.

A plasmid clone, pLCMHF/UB, generously provided by Dr. O. Wiborg harbouring a human ubiquitin cDNA insert (SEQ ID: 16) was used as template and SEQ ID NO: 17 together with SEQ ID NO: 18 were used for amplification in a Polymerase Chain Reaction (PCR) (Saiki *et al.*, 1988) of the nucleotide sequence encoding amino acid residue Ile1 to Gly76 of human ubiquitin(SEQ ID: 19). The amplified DNA fragment was after digestion with the restriction endonucleases BamHI and HindIII ligated into the BamHI and HindIII sites of pTtripb (Example 1) yielding pTtripb-UB (Fig. 13) using standard procedures.

To prepare the chimeric fusion protein H6FXtripb-UB (Fig. 14, SEQ ID NO: 31) the plasmid pTtripb-UB was grown in medium scale (4 x 1 litre; 2xTY medium, 5 mM $MgSO_4$ and 100 μg ampicillin) in *E. coli* BL21 cells, as described by Studier *et al.* (1990). Exponentially growing cultures at 37°C were at OD_{600} 0.8 infected with bacteriophage lambda CE6 at a multiplicity of approximately 5. Cultures were grown at 37°C for another three hours and the cells harvested by centrifugation. Cells were resuspended in 150 ml of 0.5 M NaCl, 10 mM Tris-HCl pH 8, and 1 mM EDTA pH 8. Phenol (100 ml adjusted to pH 8) was added and the mixture sonicated to extract the total protein. Protein was precipitated from the phenol phase by 2.5 volumes of ethanol and centrifugation. The protein pellet was dissolved in a buffer containing 6 M guanidinium chloride, 50 mM Tris-HCl pH 8 and 0.1 M dithioerythriol. Following gel filtration on Sephadex G-25 (Pharmacia, Sweden) into 8 M Urea, 1 M NaCl, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol, the crude protein preparation was applied to a Ni^{2+} activated NTA-agarose column for purifi-

cation (Hochuli *et al.*, 1988) and refolding of the fusion protein H6FXtripb-UB.

Synthesis and charging of the Ni^{2+} activated NTA-agarose matrix is described in Example 2. All buffers for liquid chromatography were degassed prior to use. The fusion protein H6FXtripb-UB was refolded by removing the urea and 2-mercaptoethanol from buffer II in a gradient over 5 column volumes into 50 mM Tris-HCl pH 8 and 0.5 M NaCl. After completion of the refolding procedure the H6FXtripb-UB fusion protein was eluted from the Ni^{2+}NTA-agarose columns with a buffer containing 0.5 M NaCl, 50 mM Tris-HCl, 25 mM EDTA pH 8 and gel filtrated on a Sephadex G50 column (Pharmacia) into 0.1 M Sodium borate pH 9 buffer for chemical cross-linking analysis with DMSI.

The cross-linking analysis experiment was designed both to analyze the oligomeric status of the chimeric fusion protein and the thermal stability of the presumed fusion protein trimer as described in Example 2: Samples of 15 µl H6FXtripb-UB fusion protein, at approximately 1.0 mg/ml concentration, were pre-incubated 10 min. at either 37°C, 50°C, 60°C, or 70°C before addition of 2 µl DMSI (20 mg/ml). The reactions were allowed to proceed for 15 min. before quenching by addition of 5 µl of 3 M Tris-HCl pH9.1 and the reaction mixtures were allowed to cool to room temperature. SDS-PAGE analysis of reduced samples (Fig. 12) showed, **(1)** that the fusion protein H6FXtripb-UB is a trimer in solution (monomer at 17 kDa, dimer at 35 kDa, and trimer at 43 kDa) and **(2)** that a substantial amount of trimer molecules is present even at 70°C. The appearance of other larger cross-linking products is probably due to cross-linking of trimers via the ubiquitin part of the fusion protein.

EXAMPLE 4

Design and construction of trimerised and hexamerized CEA6 scFv antibodies scFv(CEA6)-TRIPB, TRIPB-scFv(CEA6) and scFv(CEA6)-TRIPB-scFv(CEA6).

A plasmid clone, pUC19MCH/CEA6, generously provided by Dr. Kevin Pritchard, Cambridge Antibody Technology Ltd., Melbourn, UK, harbouring a nucleotide sequence (SEQ ID: 20) encoding the CEA6 antibody in single-chain Fv (scFv) format, followed in sequence by a "myc tag" (which is a general purification/detection handle), was used as template in Polymerase Chain Reactions (PCR) (Saiki *et al.*, 1988) in which the nucleotide sequence encoding the scFv + myc tag was amplified using the primer pairs (SEQ ID: 21 and SEQ ID: 22) and (SEQ ID: 21 and SEQ ID: 23) to generate PCR fragments "A" and "B".

PCR fragment "A" was treated with restrictions enzymes BamHI and KpnI and the resulting fragment was inserted into BglII/KpnI cut pTripb (Example 1) to obtain the vector pTH6FXscFv(CEA6)-tripb (Fig. 15) encoding the H6FXscFv(CEA6)-TRIPB fusion protein (Fig. 16). PCR fragment "B" was treated with restriction enzymes BamHI and HindIII and the resulting fragment was inserted into BamHI and HindIII cut pTripb (Example 1) to obtain the vector pTH6FXtripb-scFv(CEA6) (Fig. 17) encoding the H6FXTRIPB-scFv(CEA6) fusion protein (Fig.18, SEQ ID NO: 33) using standard procedures.

To generate the expression vector pTH6FXscFv(CEA6)-tripb-scFv(CEA6) (Fig. 19) encoding the H6FXscFv(CEA6)-TRIPB-scFv(CEA6) fusion protein (Fig. 20, SEQ ID NO: 34) the insert in the vector pTH6FXtripb-scFv(CEA6) was excised using restriction enzymes BamHI and HindIII and inserted into the vector pTH6FXscFv(CEA6)-tripb, which had been treated with restriction enzymes BamHI and HindIII.

To prepare the chimeric fusion proteins H6FXscFv(CEA6)-TRIPB (SEQ ID NO: 32), H6FXTRIPB-scFv(CEA6) (SEQ ID NO: 33) and H6FXscFv(CEA6)-TRIPB-scFv(CEA6) (SEQ ID NO: 34) the plasmids pTH6FXscFv(CEA6)-TRIPB, pTH6FXtripb-scFv(CEA6) and pTH6FXscFv(CEA6)-tripb- scFv(CEA6) were grown in small scale (1 litre; 2xTY medium, 5 mM MgSO4 and 100 μg ampicillin) in E. coli BL21 cells, as described by Studier *et al.* (1990). Exponentially growing cultures at 37°C were at OD_{600} 0.8 infected with bacteriophage lambda CE6 at a multiplicity of approximately 5. Cultures were grown at 37°C for another three hours and the cells harvested by centrifugation. Cells were resuspended in 50 ml of 0.5 M NaCl, 50 mM Tris-HCl pH 8, and 1 mM EDTA pH 8. Phenol (50 ml adjusted to pH 8) was added to each and the mixtures were sonicated to extract total protein. After clarification by centrifugation (25 minutes at 10.000 g) crude protein fractions were precipitated from the phenol phases by addition of 2.5 volumes of ethanol and centrifugation. Protein pellets were dissolved in a buffer (15-25 ml) containing 6 M guanidinium chloride, 50 mM Tris-HCl pH 8 and 0.1 M dithioerythriol. Following gel filtration on Sephadex G-25 (Pharmacia, Sweden) into 8 M Urea, 1 M NaCl, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol, the crude protein preparations were applied to Ni^{2+} activated NTA-agarose columns (75 ml column volume) for purification (Hochuli *et al.*, 1988). Washing buffer (6 M guanidine-HCl, 50 mM Tris-HCl pH 8 and 10 mM 2-mercaptoethanol) was then flowed through the columns until stable baselines were obtained. Virtually pure fusion proteins could then be eluted by applying a pH gradient to each column (1000 ml gradient in 8 M urea and 10 mM 2-mercaptoethanol obtained by linear (per volume) mixing of solutions containing 50 mM sodium di-hydrogenphosphate (pH 5 buffer) and 50 mM di-sodium hydrogenphosphate (pH 8 buffer).

In preparation for in vitro refolding by the method of Thøgersen *et al.* (WO 94/18227) 20 mg of each purified fusion protein were mixed in suspensions in refolding "buffer B" (described below) with aliquots of suspensions of Ni^{2+} acti-

vated NTA-agarose matrix sufficient to generate columns of about 75 ml packed bed volume. Each fusion protein was then subjected to the iterative refolding procedure as described for plasminogen kringle 4 in the Thøgersen *et al.* patent application (WO 94/18227), except that refolding of the scFv containing fusion proteins was carried out at 10°C using a buffer containing 0.5 M NaCl, 50 mM Tris-HCl pH 8, 2 mM glutathione and 0.2 mM oxidized glutathione as "buffer A" and a buffer containing 8 M urea, 1 M NaCl, 50 mM Tris-HCl pH 8 and 2 mM glutathione as "buffer B".

After completion of the refolding procedure each column was washed with 300 ml buffer containing 0.5 M NaCl and 50 mM Tris-HCl pH 8 to wash away glutathione. The refolded fraction of each protein was then eluted from the NTA-agarose matrix by addition of 20 mM EDTA to the elution buffer. After addition of solid urea to achieve a final concentration of about 8 M to each protein sample and dilution or dialysis to reduce NaCl concentrations to below 5 mM, final purification of each correctly folded fusion protein product was then accomplished by ion exchange chromatography (S-Sepharose, Pharmacia, 1,6 (i.d.) by 90 centimeter column in a buffer containing 8 M urea, 5 mM Tris-HCl (from 1 M stock solution at pH 8) and 25 mM sodium acetate (from 1 M stock solution at pH 5), eluted at 2 ml/min). After dialysis against aqueous buffers (e.g. phosphate buffered saline) each pure and correctly refolded fusion protein was recovered in yields of 2-6 mg per litre of culture grown. Each protein may be shown by analytical gel filtration, chemical cross-linking analysis, by in vitro affinity measurements and by in vivo efficacy to form a stable homotrimeric molecular complex: The oligomeric status of the H6FXtripb-scFv-(CEA6) fusion protein was analyzed by chemical cross-linking analysis with DMSI: In parallel experiments, samples of H6FXtripb-scFv-(CEA6) at 0.34 mg/ml and TN123 at 0.28 mg/ml in 0.1 M Sodium borate were incubated at room temperature with increasing amounts (0 - 40 μg in 12 μl in total) of DMSI for 30 min. Reactions were quenched by addition of 5 μl 3M Tris-HCl pH 9 and the samples analyzed by

SDS-PAGE under reducing conditions (Fig. 21). Like tetranectin, the H6FXtripb-scFV-(CEA6) fusion protein, of approximately 38 kDa, is hereby shown to be a trimer in solution.

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SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT
(A) NAME: Thøgersen, Hans Christian
(B) STREET: Ristrupvej 41
(C) CITY: Mundelstrup
(D) STATE OR PROVINCE:
(E) COUNTRY: Denmark
(F) POSTAL CODE: 8381

(ii) TITLE OF THE INVENTION: Trimerising module

(iii) NUMBER OF SEQUENCES: 34

(iv) COMPUTER-READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(v) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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(2) INFORMATION FOR SEQ ID NO:3:

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(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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(2) INFORMATION FOR SEQ ID NO:4:

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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(2) INFORMATION FOR SEQ ID NO:5:

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(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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Val
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(C) STRANDEDNESS: single
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65                  70                  75                  80
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            100                 105                 110
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        115                 120                 125
Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro
    130                 135                 140
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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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39

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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(2) INFORMATION FOR SEQ ID NO:10:

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(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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(2) INFORMATION FOR SEQ ID NO:11:

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(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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(2) INFORMATION FOR SEQ ID NO:12:

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGAAGCTTA GACCGTCTGC AGGGC 25

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCGGATCCA TCCAGGGTAG GGTTGTGAAC ACAAAGATG 39

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTGGATCCA TCGAGGGTAG GGCCCTGCAG ACGGTC 36

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGCAGATCT TTGTGAAGAC CCTCACTGGC AAAACCATCA CCCTTGAGGT CGAGCCCAGT 60
GACACCATTG AGAATGTCAA AGCCAAAATT CAAGACAAGG AGGGTATCCC ACCTGACCGC 120
AGCGTCTGAT ATTTGCCGGC AAACAGCTGG AAGATGGACG TACTTTGTCT GACTACAATA 180
TTCAAAAGGA GTCTACTCTT CATCTTGTGT TGAGACTTCG TGGTGGT 227

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGCTGATCAC AGATCTTTGT GAAGACC 27

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGCAAGCTTG CATGCTTAGG ATCCACCACG AAGTCTCAA 39

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
 1               5                  10                  15
Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
            20                  25                  30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
        35                  40                  45
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
    50                  55                  60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGGTTCAGC TGCAGCAGTC AGGGGCTGAG GTGAAGAAGC CTGGGTCCTC GGTGAAGGTC 60

TCCTGCAAGG CTTCTGGAGG CACCTTCAGC AACTCTCCTA TCAACTGGCT GCGACAGGCC 120
CCCGGACAAG GGCTTGAGTG GATGGGAAGT ATCATCCCTT CCTTTGGTAC AGCAAACTAC 180
GCTCAGAAGT TCCAGGGCAG ACTCACGATT ACCGCGGACG AATCCACGAG CACAGCCTAC 240
ATGGAGCTGA GCAGCCTGAG ATCTGAGGAC ACGGCCGTGT ATTACTGTGC GGGGCGGAGC 300
CACAACTACG AACTCTACTA TTACTACATG GACGTCTGGG GCCAGGGGAC AATGGTCACC 360
GTCTCGAGTG GTGGAGGCGG TTCAGGCGGA GGTGGCAGCG GCGGTGGCGG ATCGGACATC 420
CAGATGACCC AGTCTCCTTC CACCCTGTCT GCATCTATTG GAGACAGAGT CACCATCACC 480
TGCCGGGCCA GTGAGGGTAT TTATCACTGG TTGGCCTGGT ATCAGCAGAA GCCAGGGAAA 540
GCCCCTAAAC TCCTGATCTA TAAGGCCTCT AGTTTAGCCA GTGGGGCCCC ATCAAGGTTC 600
AGCGGCAGTG GATCTGGGAC AGATTTCACT CTCACCATCA GCAGCCTGCA GCCTGATGAT 660
TTTGCAACTT ATTACTGCCA ACAATATAGT AATTATCCGC TCACTTTCGG CGGAGGGACC 720
AAGCTGGAGA TCAAACGTGC GGCCGCAGAA CAAAAACTCA TCTCAGAAGA GGATCTGAAT 780
GGGGCC 786

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGTGGATCCC AGGTTCAGCT GCAGC 25

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCGGTACCG GCCCCATTCA GATCC 25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCCAAGCTTA GGCCCCATTC AGATCC 26

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Met Val Arg Ala Asn Lys Arg Asn Glu Ala Leu Arg Ile Glu Ser Ala
 1               5                  10                  15
Leu Leu Asn Lys Ile Ala Met Leu Gly Thr Glu Lys Thr Ala Glu Gly
            20                  25                  30
Gly Ser His His His His His His Gly Ser Ile Glu Gly Arg Gly Glu
        35                  40                  45
Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
    50                  55                  60
Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
65                  70                  75                  80
Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
                85                  90                  95
Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
            100                 105                 110
Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg Gly
        115                 120                 125
Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
    130                 135                 140
Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
145                 150                 155                 160
Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
                165                 170                 175
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
            180                 185                 190
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
        195                 200                 205
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
    210                 215                 220
Phe Gly Ile Val
225
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Met Gly Ser His His His His His His Gly Ser Ile Glu Gly Arg Gly
 1               5                  10                  15
Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp
            20                  25                  30
Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr
        35                  40                  45
Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
    50                  55                  60
```

```
Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe
65                  70                  75                  80
Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg
                85                  90                  95
Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu
            100                 105                 110
Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu
        115                 120                 125
Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly
    130                 135                 140
Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro
145                 150                 155                 160
Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn
                165                 170                 175
Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys
            180                 185                 190
Gln Phe Gly Ile Val
        195
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Met Gly Ser His His His His His His Gly Ser Ile Glu Gly Arg Gly
 1               5                  10                  15
Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp
            20                  25                  30
Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr
        35                  40                  45
Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
    50                  55                  60
Val
65
```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Val
 1               5                  10                  15
Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
            20                  25                  30
```

```
Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
        35                  40                  45
Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
    50                  55                  60
Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg Gly
65                  70                  75                  80
Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
                85                  90                  95
Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
            100                 105                 110
Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
        115                 120                 125
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
    130                 135                 140
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
145                 150                 155                 160
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
                165                 170                 175
Phe Gly Ile Val
            180
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser
 1               5                  10                  15
Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala
            20                  25                  30
Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg
        35                  40                  45
Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala
    50                  55                  60
Leu Gln Thr Val Ser Leu Lys Gly Ser
65                  70
```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser
 1               5                  10                  15
```

```
Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala
            20                  25                  30
Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg
        35                  40                  45
Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala
    50                  55                  60
Leu Gln Thr Gly Ser
65
```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Met Gly Ser His His His His His His Gly Ser Ile Glu Gly Arg Ala
 1               5                  10                  15
Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe
            20                  25                  30
Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys
        35                  40                  45
Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn
    50                  55                  60
Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu
65                  70                  75                  80
Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp
                85                  90                  95
Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr
            100                 105                 110
Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly
        115                 120                 125
Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro
    130                 135                 140
Tyr Ile Cys Gln Phe Gly Ile Val
145                 150
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser
 1               5                  10                  15
Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala
            20                  25                  30
```

```
Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg
        35                  40                  45
Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala
    50                  55                  60
Leu Gln Thr Gly Ser Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr
65                  70                  75                  80
Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala
                85                  90                  95
Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile
            100                 105                 110
Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn
        115                 120                 125
Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
    130                 135                 140
Ser
145
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser
 1                  5                  10                  15
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
            20                  25                  30
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Ser
        35                  40                  45
Pro Ile Asn Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
    50                  55                  60
Gly Ser Ile Ile Pro Ser Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
65                  70                  75                  80
Gln Gly Arg Leu Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
                85                  90                  95
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
            100                 105                 110
Ala Gly Arg Ser His Asn Tyr Glu Leu Tyr Tyr Tyr Tyr Met Asp Val
        115                 120                 125
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
    130                 135                 140
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
145                 150                 155                 160
Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr
                165                 170                 175
Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln
            180                 185                 190
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu
        195                 200                 205
Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    210                 215                 220
```

```
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
225                 230                 235                 240
Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr
                245                 250                 255
Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu
            260                 265                 270
Glu Asp Leu Asn Gly Ala Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys
        275                 280                 285
Lys Ile Val Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu
    290                 295                 300
Glu Leu Lys Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu
305                 310                 315                 320
Lys Glu Gln Gln Ala Leu Gln Thr Gly Ser
                325                 330
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser
 1                5                  10                  15
Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala
            20                  25                  30
Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg
        35                  40                  45
Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala
    50                  55                  60
Leu Gln Thr Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val
65                  70                  75                  80
Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
                85                  90                  95
Thr Phe Ser Asn Ser Pro Ile Asn Trp Leu Arg Gln Ala Pro Gly Gln
            100                 105                 110
Gly Leu Glu Trp Met Gly Ser Ile Ile Pro Ser Phe Gly Thr Ala Asn
        115                 120                 125
Tyr Ala Gln Lys Phe Gln Gly Arg Leu Thr Ile Thr Ala Asp Glu Ser
    130                 135                 140
Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
145                 150                 155                 160
Ala Val Tyr Tyr Cys Ala Gly Arg Ser His Asn Tyr Glu Leu Tyr Tyr
                165                 170                 175
Tyr Tyr Met Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
            180                 185                 190
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
        195                 200                 205
Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp
    210                 215                 220
Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu
225                 230                 235                 240
```

```
Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
                245                 250                 255
Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly Ser
            260                 265                 270
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
        275                 280                 285
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr
    290                 295                 300
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln
305                 310                 315                 320
Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
                325                 330
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 592 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Met Gly Ser His His His His His His Gly Ser Ile Gln Gly Arg Ser
 1                5                  10                  15
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
            20                  25                  30
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Ser
        35                  40                  45
Pro Ile Asn Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
    50                  55                  60
Gly Ser Ile Ile Pro Ser Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
65                  70                  75                  80
Gln Gly Arg Leu Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
                85                  90                  95
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
            100                 105                 110
Ala Gly Arg Ser His Asn Tyr Glu Leu Tyr Tyr Tyr Tyr Met Asp Val
        115                 120                 125
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
    130                 135                 140
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
145                 150                 155                 160
Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr
                165                 170                 175
Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln
            180                 185                 190
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu
        195                 200                 205
Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    210                 215                 220
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
225                 230                 235                 240
Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr
                245                 250                 255
```

```
Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu
            260                 265                 270
Glu Asp Leu Asn Gly Ala Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys
        275                 280                 285
Lys Ile Val Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu
    290                 295                 300
Glu Leu Lys Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu
305                 310                 315                 320
Lys Glu Gln Gln Ala Leu Gln Thr Gly Ser Gln Val Gln Leu Gln Gln
                325                 330                 335
Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys
            340                 345                 350
Lys Ala Ser Gly Gly Thr Phe Ser Asn Ser Pro Ile Asn Trp Leu Arg
        355                 360                 365
Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ser Ile Ile Pro Ser
    370                 375                 380
Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Leu Thr Ile
385                 390                 395                 400
Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
                405                 410                 415
Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Gly Arg Ser His Asn
            420                 425                 430
Tyr Glu Leu Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Gln Gly Thr Met
        435                 440                 445
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    450                 455                 460
Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
465                 470                 475                 480
Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly
                485                 490                 495
Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
            500                 505                 510
Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser
        515                 520                 525
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
    530                 535                 540
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser
545                 550                 555                 560
Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
                565                 570                 575
Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
            580                 585                 590
```

CLAIMS

1. A monomer polypeptide construct comprising at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, said TTSE being capable of forming a stable complex with two other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23, the sequences of which are shown in SEQ ID NOs: 24-27.

2. A monomer polypeptide construct comprising at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, said TTSE being capable of forming a stable complex with two other TTSEs, said at least one heterologous moiety being one which does not exclusively facilitate expression and/or purification of the monomer polypeptide construct.

3. A monomer polypeptide construct according to claim 1 or 2, wherein the stable complex includes a triple alpha helical coiled coil.

4. A monomer polypeptide construct according to any of the preceding claims, wherein the heterologous moiety is selected from the group consisting of a ligand binding structure; a toxin; a detectable label; an *in situ* activatable substance; an enzyme; a radioactive moiety; a cytokine; a non-proteinaceous polymer such as a polymeric alkaloid, a polyalcohol, a polysaccharide, a lipid and a polyamine; a photo cross-linking agent; and a group facilitating conjugation of the monomer polypeptide construct to a target.

5. A monomer polypeptide construct according to any of the preceding claims, which comprises 2 TTSEs which are covalently linked by a spacer moiety which allows both of the 2 TTSEs to take part in complex formation with a third TTSE not being part of the monomer polypeptide construct.

6. A monomer polypeptide construct according to claim 5, wherein the spacer moiety has a length and a conformation which favours complex formation involving both of the two TTSEs which are covalently linked by the spacer moiety.

7. A monomer polypeptide construct according to claim 5 or 6, wherein the spacer moiety is a polypeptide fragment.

8. A monomer polypeptide construct according to any of claims 1-4, which comprises one single TTSE.

9. A monomer polypeptide construct according to any of the preceding claims, wherein the TTSE is derived from human tetranectin, murine tetranectin, C-type lectin of bovine cartilage, or C-type lectin of shark cartilage.

10. A monomer polypeptide construct according to claim 9, wherein the TTSE comprises a polypeptide sequence which has at least 68% sequence identity with the consensus sequence shown in Fig. 2.

11. A monomer polypeptide construct according to claim 10, wherein the sequence identity with the consensus sequence is at least 75%, such as at least 81%, at least 87%, or at least 92%.

12. A monomer polypeptide construct according to any of claims 9-11, wherein at least one amino acid residue selected from the group consisting of amino acid residue nos. 6, 21, 22, 24, 25, 27, 28, 31, 32, 35, 39, 41, 42, is/are substituted by any non-helix breaking amino acid residue, the amino acid residue numbering referring to amino acid residues in SEQ ID NO: 7.

13. A monomer polypeptide construct according to any of the preceding claims, wherein the at least one TTSE comprises a repeated heptad having the formula a-b-c-d-e-f-g (N to C),

wherein residues a and d generally are hydrophobic amino acids.

14. A monomer polypeptide construct according to claim 13, wherein heptad is repeated 3 times and wherein the last occurrence of the heptad has a glutamine residue corresponding to residues a and d.

15. A monomer polypeptide construct according to any of the preceding claims, wherein the heterologous moiety is covalently linked to the TTSE by via a peptide bond to the N- or C-terminus of the TTSE peptide chain, via a peptide bond to a side chain in the TTSE or via a bond to a cysteine residue.

16. A monomer polypeptide construct according to any of the preceding claims which lacks any free amino and/or carboxy groups.

17. A monomer polypeptide construct according to any of the preceding claims which lacks substantial of tetranectin which is encoded by exon 3 and/or lacks substantial part of tetranectin which is encoded by exon 1.

18. A monomer polypeptide construct according to any of the preceding claims comprising two heterologous moieties which are linked via peptide bonds to the N- and C-terminus, respectively.

19. A monomer polypeptide construct according to any of the preceding claims which is constructed so as to disfavour formation of complexes between identical TTSEs.

20. An oligomer which is comprised of two monomer polypeptide constructs according to any of claims 1-19, and which comprises at least three TTSE's, or which is comprised of three monomer polypeptide constructs according to any of claims 1-4 or 8-19.

21. An oligomer according to claim 20 which is stable in the temperature range 50-70°C.

22. An oligomer according to claim 20 or 21, which comprises at least one heterologous moiety which is positioned N-terminally to a TTSE and at least one heterologous moiety which is positioned C-terminally to a TTSE.

23. An oligomer according to claim 22, wherein the at least one heterologous moiety which is positioned N-terminally to a TTSE and the at least one heterologous moiety which is positioned C-terminally to a TTSE are part of the same monomeric polypeptide construct.

24. An oligomer according to claim 22, wherein the at least one heterologous moiety which is positioned N-terminally to a TTSE and the at least one heterologous moiety which is positioned C-terminally to a TTSE are part of two separate monomeric polypeptide constructs.

25. An oligomer according to any of claims 20-24, wherein each monomer polypeptide construct is designed so as to disfavour formation of trimers including two monomer polypeptide constructs having identical TTSEs.

26. A method of preparing a monomer polypeptide construct according to any of claims 1-19, the method comprising

- isolating the monomer polypeptide construct from a culture comprising a host cell which carries and expresses a nucleic acid fragment which encodes the monomer polypeptide construct,

- synthesizing, by means of chemical peptide synthesis, the monomer polypeptide construct and subsequently isolating the monomer polypeptide construct from the reaction mixture,

- preparing a TTSE in a culture comprising a host cell which carries and expresses a nucleic acid fragment which encodes the TTSE, subsequently linking covalently at least one heterologous moiety to the TTSE, and thereafter isolating the resulting monomer polypeptide construct, or

- synthesizing, by means of chemical peptide synthesis, a TTSE, subsequently linking covalently at least one heterologous moiety to the TTSE, and thereafter the isolating the resulting monomer polypeptide construct from the reaction mixture,

and optionally subjecting the monomer polypeptide construct to further processing.

27. A method for preparing a dimeric oligomer according to claim 20 which comprises

- admixing a monomer polypeptide construct according to any of claims 1-19 which includes two TTSEs (construct 1) with a monomer polypeptide construct according to any of claims 1-4 or 8-19 which includes only one TTSE (construct 2),

- effecting the two TTSE's of construct 1 to complex with the TTSE of construct 2, and

- isolating the resulting dimer and optionally subjecting the dimer to further processing.

28. A method for preparing a trimeric oligomer according to claim 20 which comprises

- admixing three monomer polypeptide constructs according to any of claims 1-19 with each other,

- effecting complex formation between one TTSE of each monomer polypeptide construct, and

- isolating the resulting trimer and optionally subjecting the trimeric oligomer to further processing.

29. A kit comprising

- a first package comprising at least one container means, each at least one container means containing a monomer polypeptide construct according to any of claims 1-19,

- a second package comprising at least one container means, each at least one container means in the second package containing a monomer polypeptide construct according to any of claims 1-19, the second package being different from the first package with respect to choice and/or number of monomer polypeptide constructs included therein, and optionally

- a third package comprising at least one container means, each at least one container means in the third package containing a monomer polypeptide construct according to any of claims 1-19, the second package being different from the first and second packages with respect to choice and/or number of monomer polypeptide constructs included therein.

30. A kit according to claim 29, wherein the at least one container means in each package contains mutually distinct monomer polypeptide constructs.

31. A kit according to claim 29 or 30, wherein all container means comprised in the kit comprises mutually distinct polypeptide constructs.

32. A nucleic acid fragment in isolated form which encodes a TTSE as defined in any of claims 1-19 or which encodes the polypeptide part of a monomer polypeptide construct according to any of claims 1-19, with the proviso that the nucleic acid fragment is different from one that encodes native members of

the tetranectin family, and that the nucleic acid fragment is different from one that encodes any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23, the sequences of which are shown in SEQ ID NOs: 24-27.

33. A replicable vector which comprises a nucleic acid fragment according to claim 32.

34. A transformed host cell, which comprises a nucleic acid fragment according to claim 32 or a replicable vector according to claim 32.

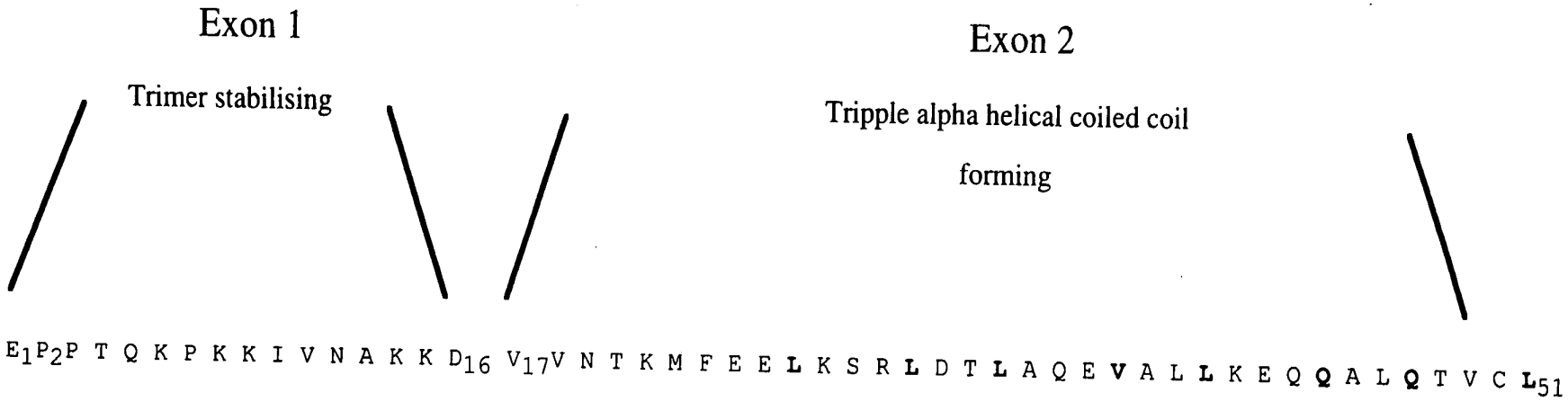

Exon 1
Trimer stabilising
Exon 2
Tripple alpha helical coiled coil
forming
E1P2P T Q K P K K I V N A K K D16 V17V N T K M F E E L K S R L D T L A Q E V A L L K E Q Q A L Q T V C L51

Fig. 1

Position																															
								d	e	f	g	**a**	b	c	**d**	e	f	g	**a**	b	c	**d**	e	f	g	**a**						
Human tetranectin	V	V	N	T	K	M	F	E	E	**L**	K	S	R	**L**	D	T	**L**	A	Q	E	**V**	A	L	**L**	K	E	Q	**Q**	A	L	**Q**	T	V	C	**L**	K
Murine tetranectin	L	V	S	S	K	M	F	E	E	**L**	K	N	R	**M**	D	V	**L**	A	Q	E	**V**	A	L	**L**	K	E	K	**Q**	A	L	**Q**	T	V	C	**L**	K
Bovine cart. protein	R	R	V	K	E	K	D	G	D	**L**	K	T	Q	**V**	E	K	**L**	W	R	E	**V**	N	A	**L**	K	E	M	**Q**	A	L	**Q**	T	V	C	**L**	R
Shark cart. protein	S	K	S	G	K	G	K	D	D	**L**	R	N	E	**I**	D	K	**L**	W	R	E	**V**	N	S	**L**	K	E	M	**Q**	A	L	**Q**	T	V	C	**L**	K
Consensus										**L**				**hy**			**L**			E	**V**			**L**	K	E		**Q**	A	L	**Q**	T	V	C	**L**	

Fig. 2

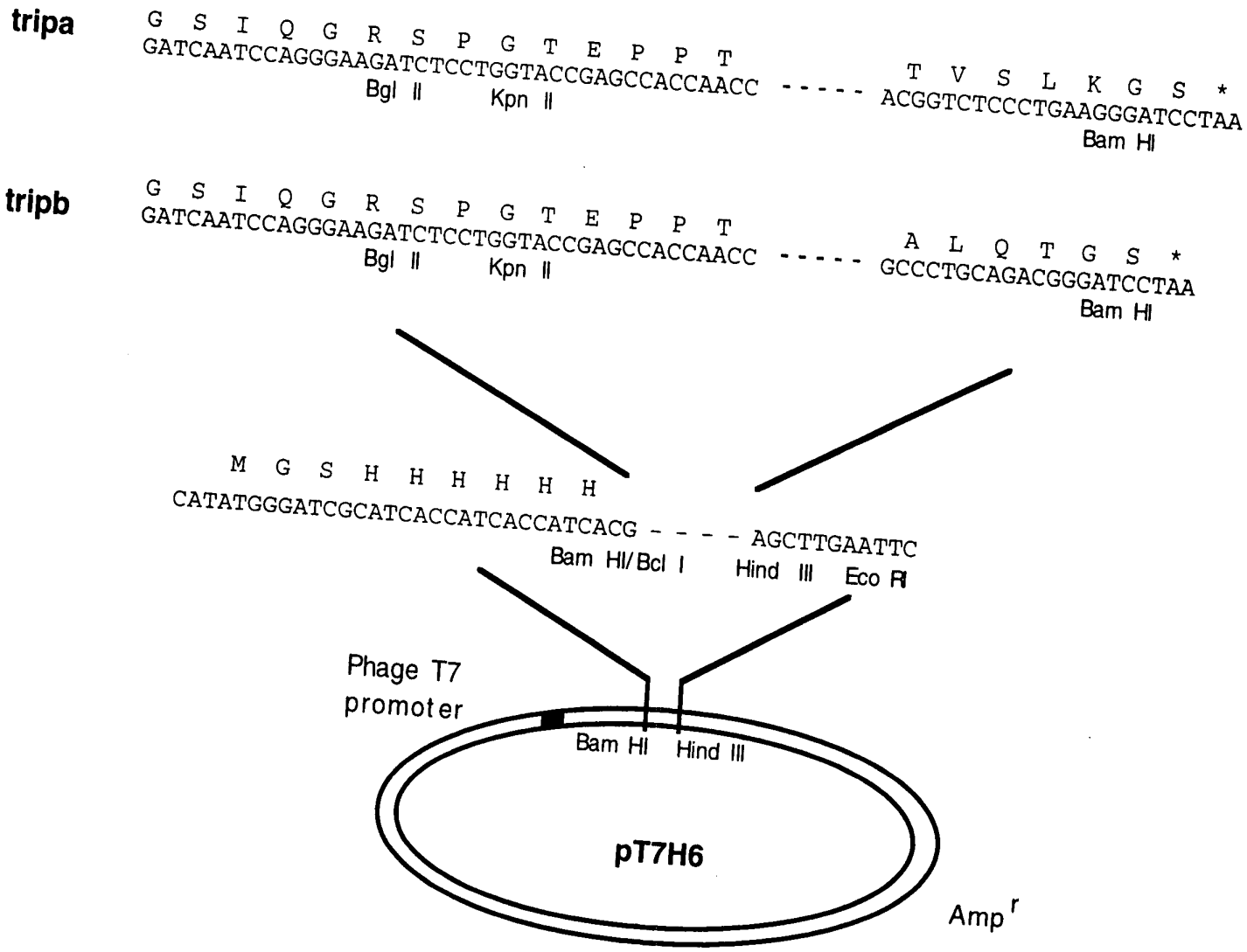

tripa
G S I Q G R S P G T E P P T
GATCAATCCAGGGAAGATCTCCTGGTACCGAGCCACCAACC - - - - - ACGGTCTCCCTGAAGGGATCCTAA
T V S L K G S *
Bgl II
Kpn II
Bam HI
tripb
G S I Q G R S P G T E P P T
GATCAATCCAGGGAAGATCTCCTGGTACCGAGCCACCAACC - - - - - GCCCTGCAGACGGGATCCTAA
A L Q T G S *
Bgl II
Kpn II
Bam HI
M G S H H H H H H
CATATGGGATCGCATCACCATCACCATCACG - - - - AGCTTGAATTC
Bam HI/Bcl I
Hind III
Eco RI
Phage T7
promoter
Bam HI
Hind III
pT7H6
Amp r

Fig. 3

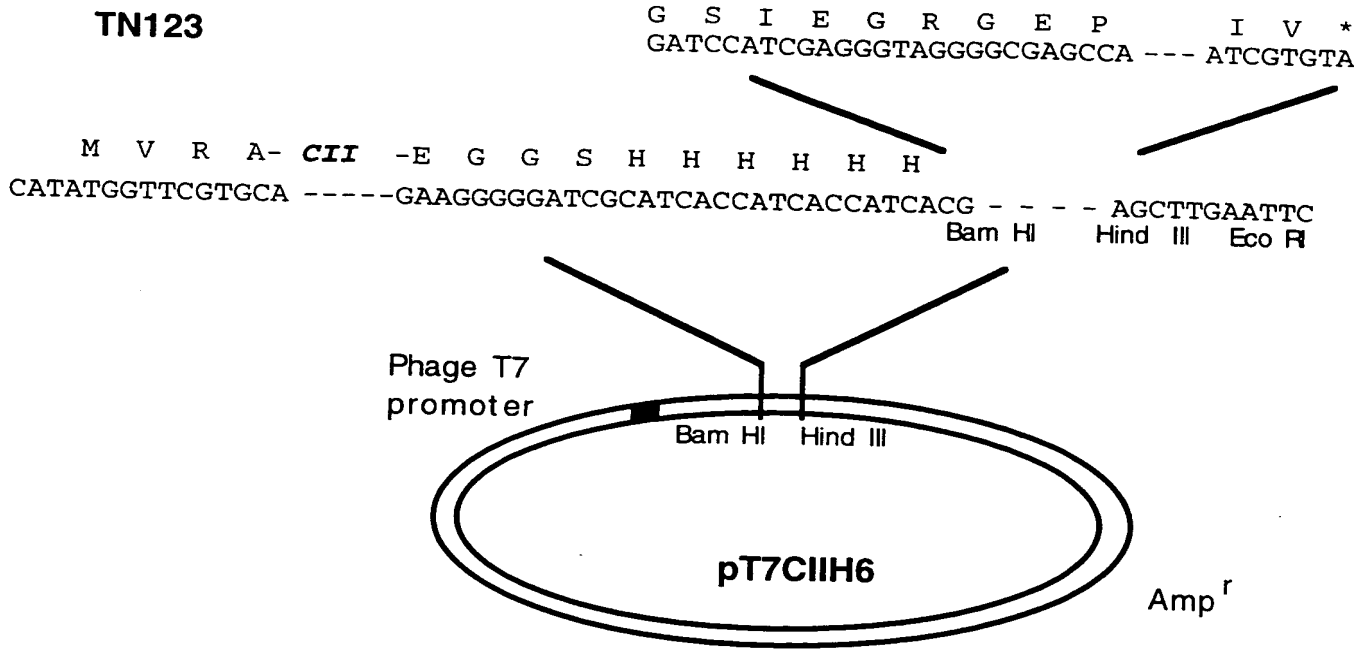
H6FXtripa fusion protein

```
 1  M G S H H H H H H G S I Q G R S P G T E P P T Q K P K K I V  30
31  N A K K D V V N T K M F E E L K S R L D T L A Q E V A L L K  60
61  E Q Q A L Q T V S L K G S *                                 73
```

H6FXtripB fusion protein

```
 1  M G S H H H H H H G S I Q G R S P G T E P P T Q K P K K I V  30
31  N A K K D V V N T K M F E E L K S R L D T L A Q E V A L L K  60
61  E Q Q A L Q T G S *                                         69
```

Fig. 4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GATCCATCGAGGGTAGGGGCGAGCCA --- ATCGTGTA
M V R A- CII -E G G S H H H H H H
CATATGGTTCGTGCA -----GAAGGGGGATCGCATCACCATCACCATCACG - - - - AGCTTGAATTC
Bam HI Hind III Eco RI
Phage T7
promoter
Bam HI Hind III
pT7CIIH6
Amp r

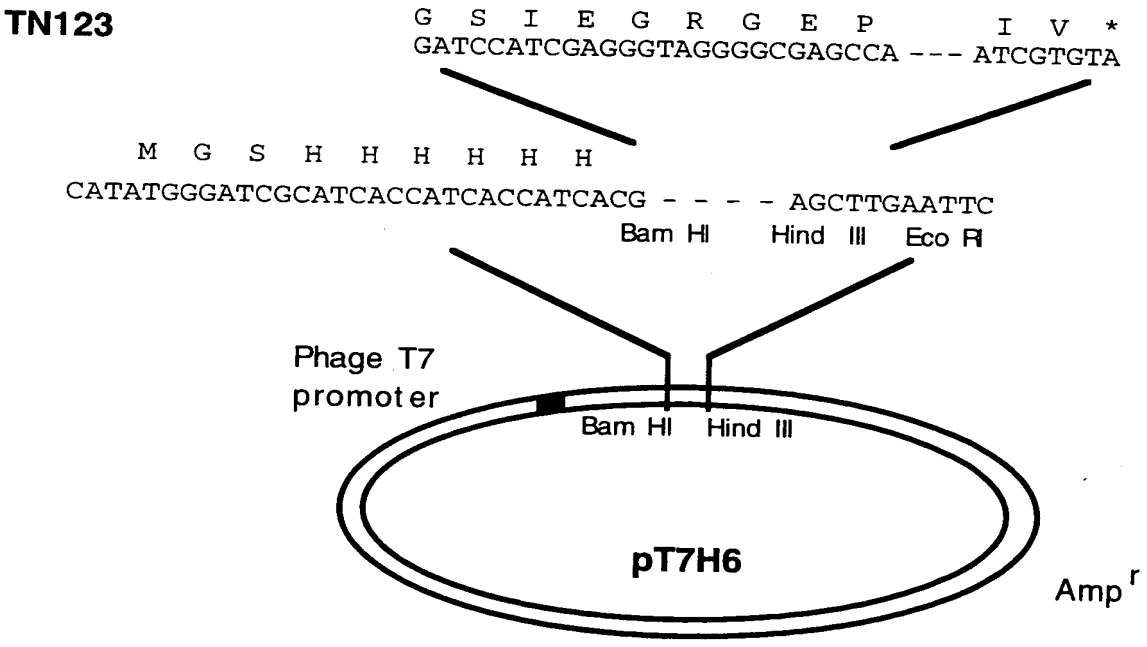

TN123
G S I E G R G E P I V *
GATCCATCGAGGGTAGGGGCGAGCCA --- ATCGTGTA
M G S H H H H H H
CATATGGGATCGCATCACCATCACCATCACG - - - - AGCTTGAATTC
Bam HI Hind III Eco RI
Phage T7
promoter
Bam HI Hind III
pT7H6
Amp r

Fig. 5

CIIH6FXTN123 fusion protein

```
  1 M V R A N K R N E A L R I E S A L L N K I A M L G T E K T A  30
 31 E G G S H H H H H H G S I E G R G E P P T Q K P K K I V N A  60
 61 K K D V V N T K M F E E L K S R L D T L A Q E V A L L K E Q  90
 91 Q A L Q T V C L K G T K V H M K C F L A F T Q T K T F H E A 120
121 S E D C I S R G G T L S T P Q T G S E N D A L Y E Y L R Q S 150
151 V G N E A E I W L G L N D M A A E G T W V D M T G A R I A Y 180
181 K N W E T E I T A Q P D G G K T E N C A V L S G A A N G K W 210
211 F D K R C R D Q L P Y I C Q F G I V *                     228
```

H6FXTN123 fusion protein

```
  1 M G S H H H H H H G S I E G R G E P P T Q K P K K I V N A K  30
 31 K D V V N T K M F E E L K S R L D T L A Q E V A L L K E Q Q  60
 61 A L Q T V C L K G T K V H M K C F L A F T Q T K T F H E A S  90
 91 E D C I S R G G T L S T P Q T G S E N D A L Y E Y L R Q S V 120
121 G N E A E I W L G L N D M A A E G T W V D M T G A R I A Y K 150
151 N W E T E I T A Q P D G G K T E N C A V L S G A A N G K W F 180
181 D K R C R D Q L P Y I C Q F G I V *                     197
```

Fig. 6

TN12

G S I E G R G E P P Q T V *
GATCCATCGAGGGTAGGGGCGAGCCACCA ---- CAGACGGTCTA

TN23

G S I Q G R V V N T G I V *
GATCCATCCAGGGTAGGGTTGTGAACACA ---- GGGATCGTGTA

TN3

G S I E G R A L Q G I V *
GATCCATCGAGGGTAGGGCCCTGCAG ---- GGGATCGTGTA

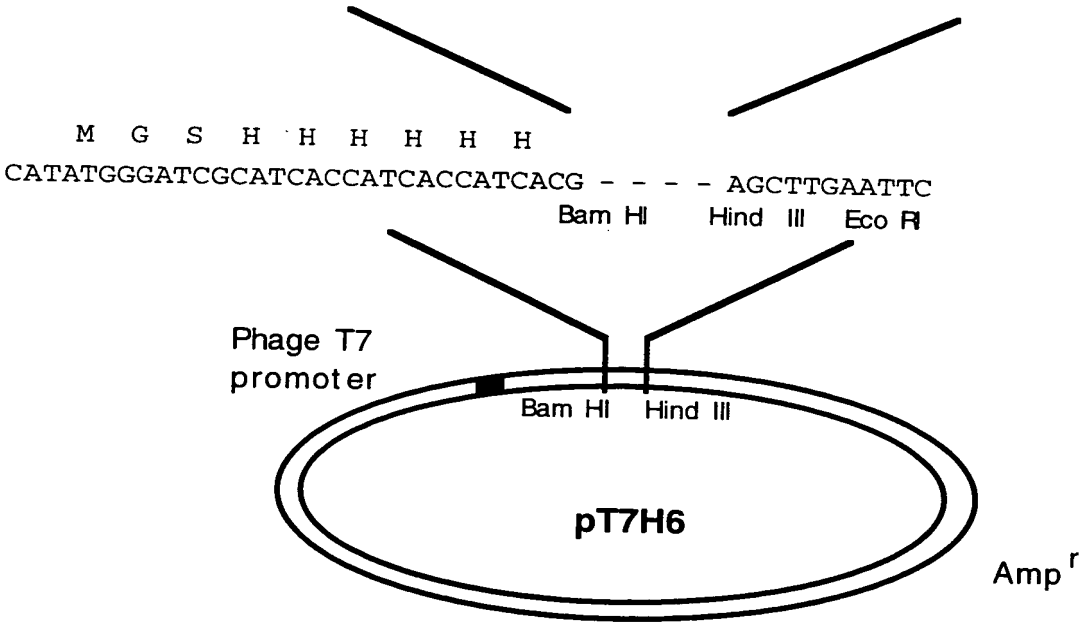


Fig. 7

H6FXTN12 fusion protein

```
  1 M G S H H H H H H G S I E G R G E P P T Q K P K K I V N A K  30
 31 K D V V N T K M F E E L K S R L D T L A Q E V A L L K E Q Q  60
 61 A L Q T V *                                                 65
```

H6FXTN23 fusion protein

```
  1 M G S H H H H H H G S I Q G R V V N T K M F E E L K S R L D  30
 31 T L A Q E V A L L K E Q Q A L Q T V C L K G T K V H M K C F  60
 61 L A F T Q T K T F H E A S E D C I S R G G T L S T P Q T G S  90
 91 E N D A L Y E Y L R Q S V G N E A E I W L G L N D M A A E G 120
121 T W V D M T G A R I A Y K N W E T E I T A Q P D G G K T E N 150
151 C A V L S G A A N G K W F D K R C R D Q L P Y I C Q F G I V 180
181 *
```

H6FXTN3 fusion protein

```
  1 M G S H H H H H H G S I E G R A L Q T V C L K G T K V H M K  30
 31 C F L A F T Q T K T F H E A S E D C I S R G G T L S T P Q T  60
 61 G S E N D A L Y E Y L R Q S V G N E A E I W L G L N D M A A  90
 91 E G T W V D M T G A R I A Y K N W E T E I T A Q P D G G K T 120
121 E N C A V L S G A A N G K W F D K R C R D Q L P Y I C Q F G 150
151 I V *                                                     152
```

Fig. 8

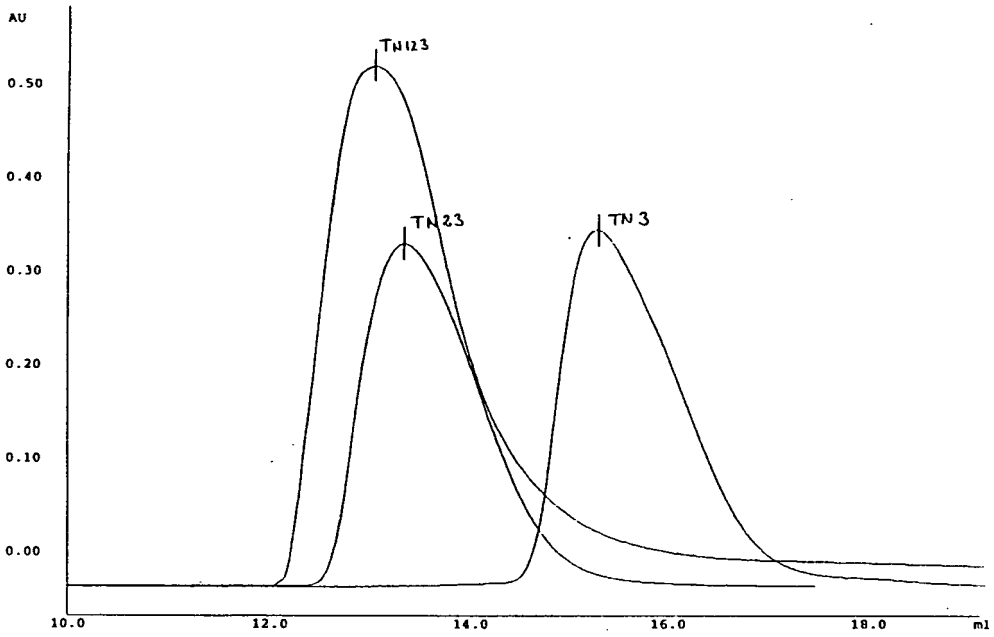


Fig. 9

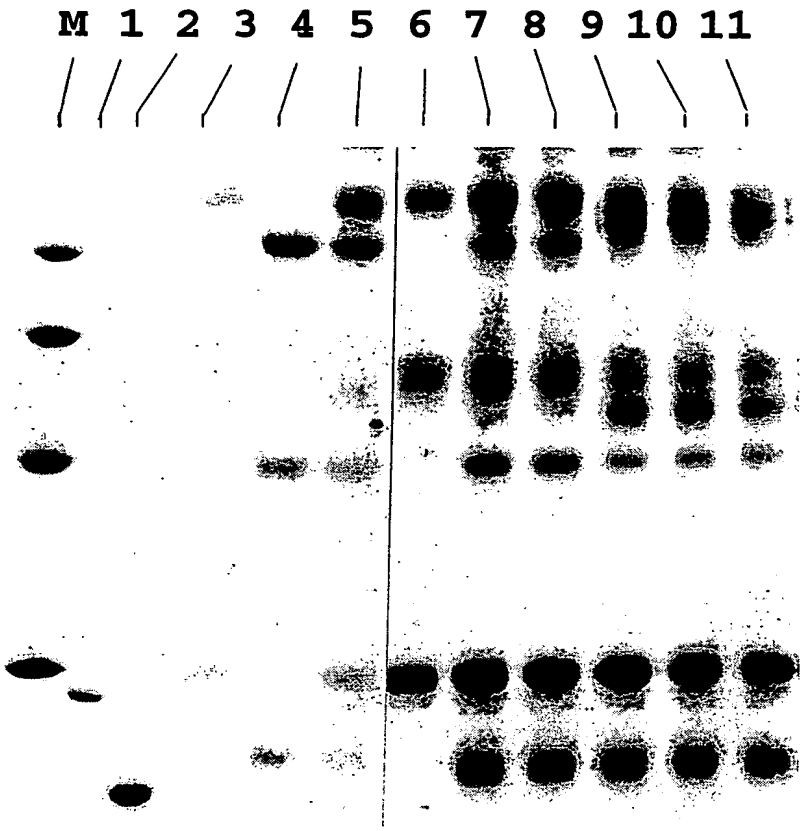


Fig. 10

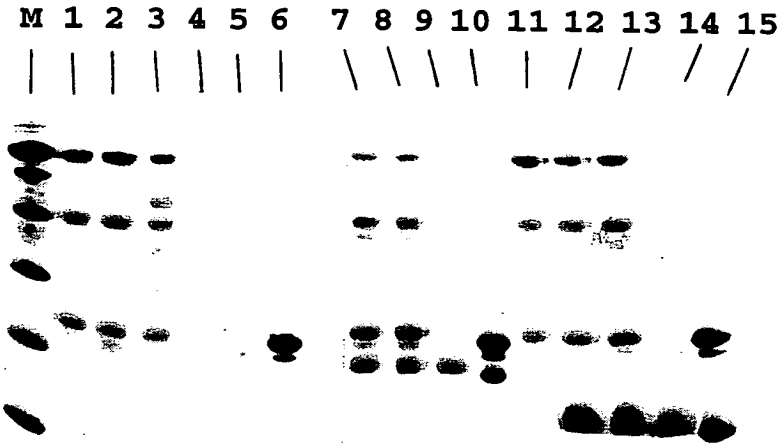


Fig. 11

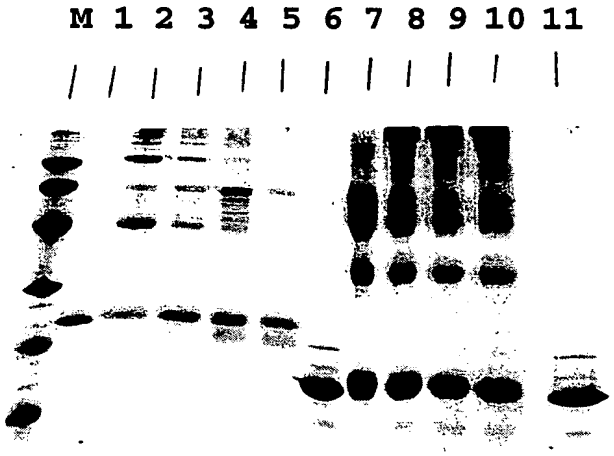


Fig. 12

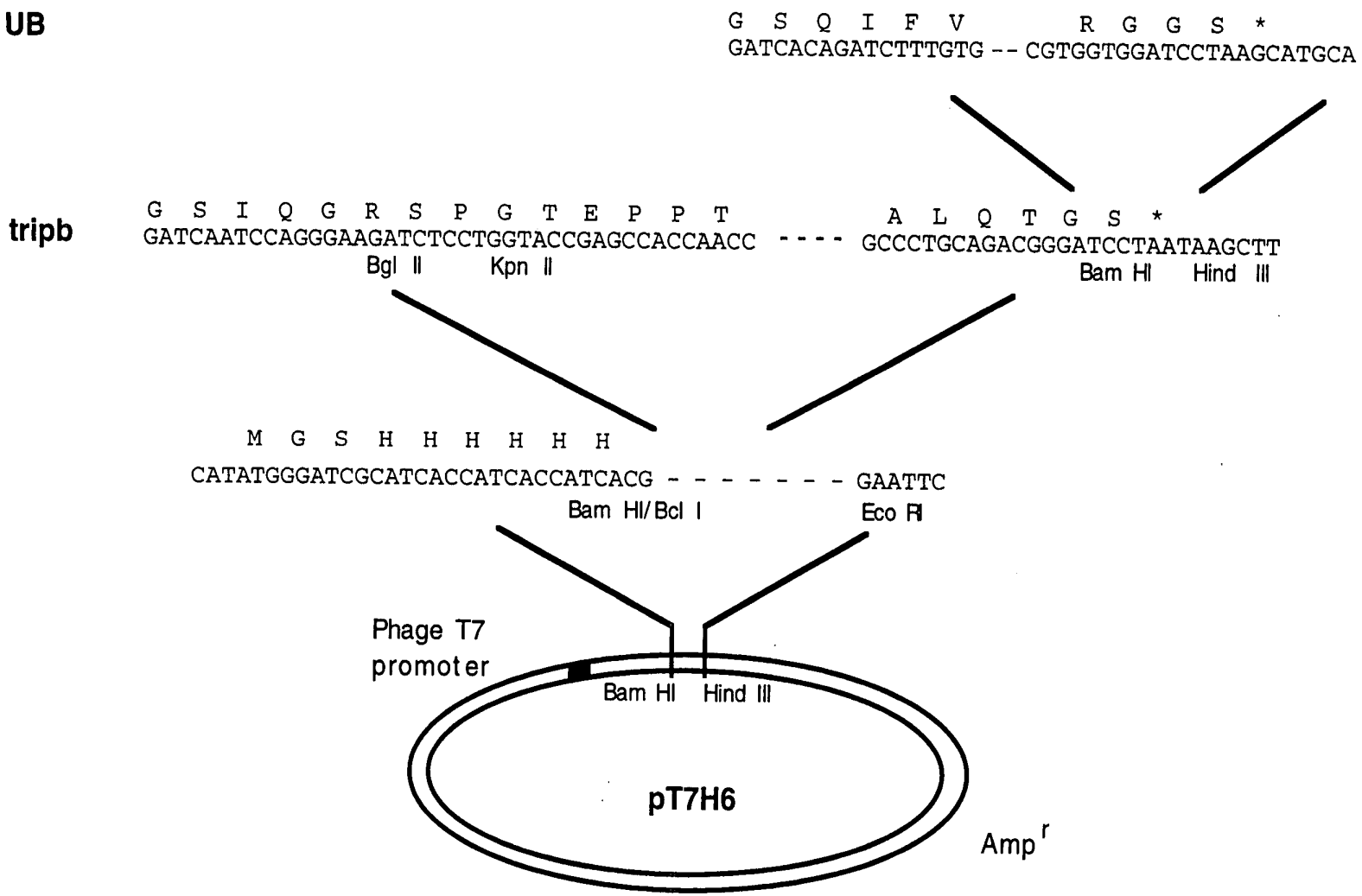

UB
G S Q I F V R G G S *
GATCACAGATCTTTGTG -- CGTGGTGGATCCTAAGCATGCA
tripb
G S I Q G R S P G T E P P T A L Q T G S *
GATCAATCCAGGGAAGATCTCCTGGTACCGAGCCACCAACC ---- GCCCTGCAGACGGGATCCTAATAAGCTT
Bgl II Kpn II Bam HI Hind III
M G S H H H H H H
CATATGGGATCGCATCACCATCACCATCACG - - - - - - - GAATTC
Bam HI/Bcl I Eco RI
Phage T7
promoter
Bam HI Hind III
pT7H6
Amp r

Fig. 13

H6FXtripb-UB fusion protein

```
  1  M G S H H H H H H G S I Q G R S P G T E P P T Q K P K K I V  30
 31  N A K K D V V N T K M F E E L K S R L D T L A Q E V A L L K  60
 61  E Q Q A L Q T G S Q I F V K T L T G K T I T L E V E P S D T  90
 91  I E N V K A K I Q D K E G I P P D Q Q R L I F A G K Q L E D 120
121  G R T L S D Y N I Q K E S T L H L V L R L R G G S * 145
```

Fig. 14

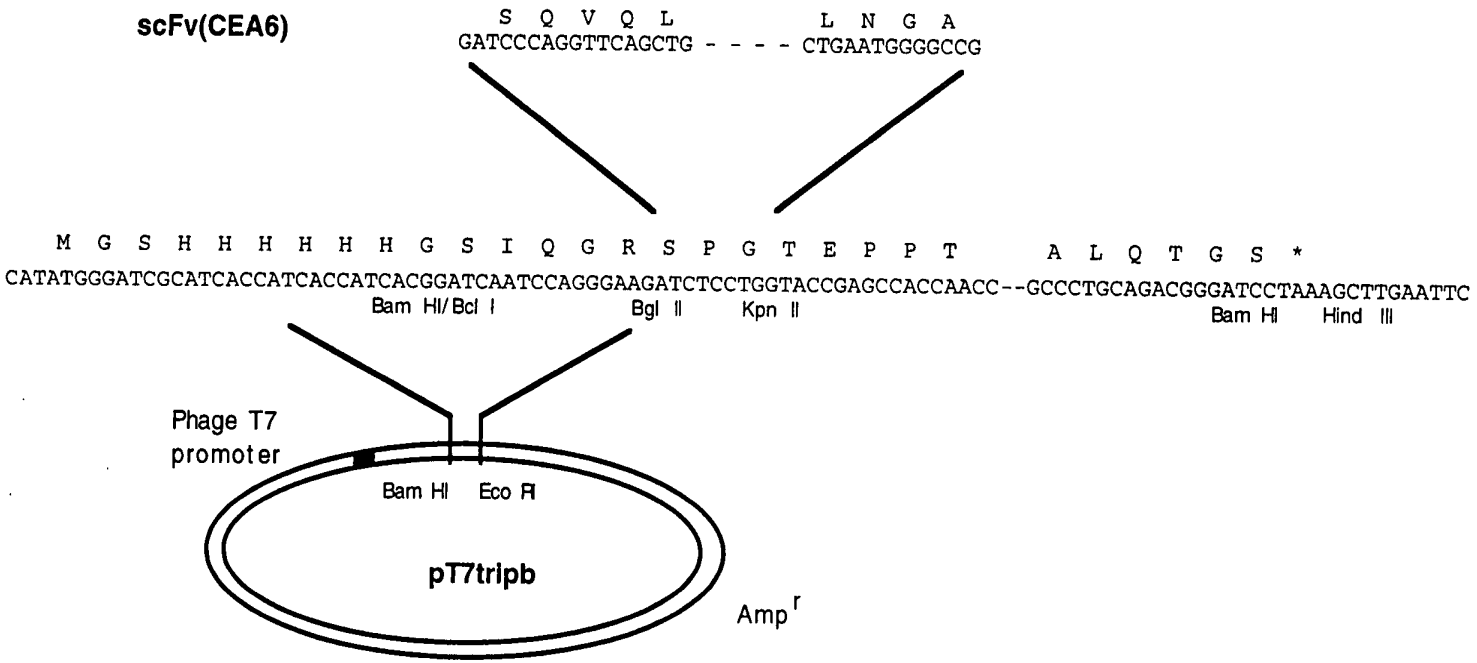
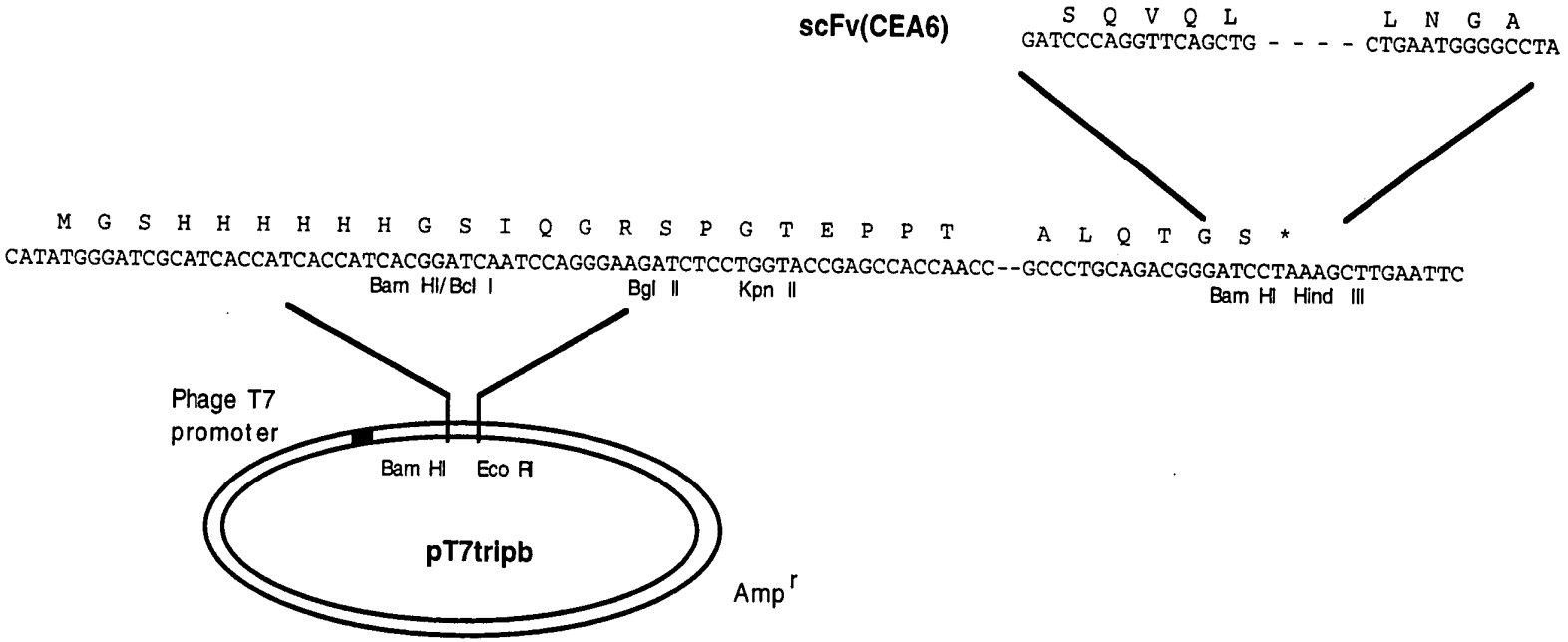

scFv(CEA6)
S Q V Q L
L N G A
GATCCCAGGTTCAGCTG - - - - CTGAATGGGGCCG
M G S H H H H H H G S I Q G R S P G T E P P T A L Q T G S *
CATATGGGATCGCATCACCATCACCATCACGGATCAATCCAGGGAAGATCTCCTGGTACCGAGCCACCAACC--GCCCTGCAGACGGGATCCTAAAGCTTGAATTC
Bam HI/Bcl I
Bgl II
Kpn II
Bam HI
Hind III
Phage T7
promoter
Bam HI
Eco RI
pT7tripb
Amp r

Fig. 15

H6FXscFv(CEA6)-tripb fusion protein

```
  1 M G S H H H H H H G S I Q G R S Q V Q L Q Q S G A E V K K P  30
 31 G S S V K V S C K A S G G T F S N S P I N W L R Q A P G Q G  60
 61 L E W M G S I I P S F G T A N Y A Q K F Q G R L T I T A D E  90
 91 S T S T A Y M E L S S L R S E D T A V Y Y C A G R S H N Y E 120
121 L Y Y Y Y M D V W G Q G T M V T V S S G G G G S G G G G S G 150
151 G G G S D I Q M T Q S P S T L S A S I G D R V T I T C R A S 180
181 E G I Y H W L A W Y Q Q K P G K A P K L L I Y K A S S L A S 210
211 G A P S R F S G S G S G T D F T L T I S S L Q P D D F A T Y 240
241 Y C Q Q Y S N Y P L T F G G G T K L E I K R A A A E Q K L I 270
271 S E E D L N G A G T E P P T Q K P K K I V N A K K D V V N T 300
301 K M F E E L K S R L D T L A Q E V A L L K E Q Q A L Q T G S 330
331 *
```

Fig. 16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S Q V Q L
GATCCCAGGTTCAGCTG - - - -
L N G A
CTGAATGGGGCCTA
M G S H H H H H H G S I Q G R S P G T E P P T
A L Q T G S *
CATATGGGATCGCATCACCATCACCATCACGGATCAATCCAGGGAAGATCTCCTGGTACCGAGCCACCAACC--GCCCTGCAGACGGGATCCTAAAGCTTGAATTC
Bam HI/Bcl I
Bgl II
Kpn II
Bam HI Hind III
Phage T7
promoter
Bam HI
Eco RI
pT7tripb
Amp r

Fig. 17

H6FXtripb-scFv(CEA6) fusion protein

```
  1 M G S H H H H H H G S I Q G R S P G T E P P T Q K P K K I V  30
 31 N A K K D V V N T K M F E E L K S R L D T L A Q E V A L L K  60
 61 E Q Q A L Q T G S Q V Q L Q Q S G A E V K K P G S S V K V S  90
 91 C K A S G G T F S N S P I N W L R Q A P G Q G L E W M G S I 120
121 I P S F G T A N Y A Q K F Q G R L T I T A D E S T S T A Y M 150
151 E L S S L R S E D T A V Y Y C A G R S H N Y E L Y Y Y Y M D 180
181 V W G Q G T M V T V S S G G G G S G G G G S G G G G S D I Q 210
211 M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H W L 240
241 A W Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F S 270
271 G S G S G T D F T L T I S S L Q P D D F A T Y Y C Q Q Y S N 300
301 Y P L T F G G G T K L E I K R A A A E Q K L I S E E D L N G 330
331 A *
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Fig. 18

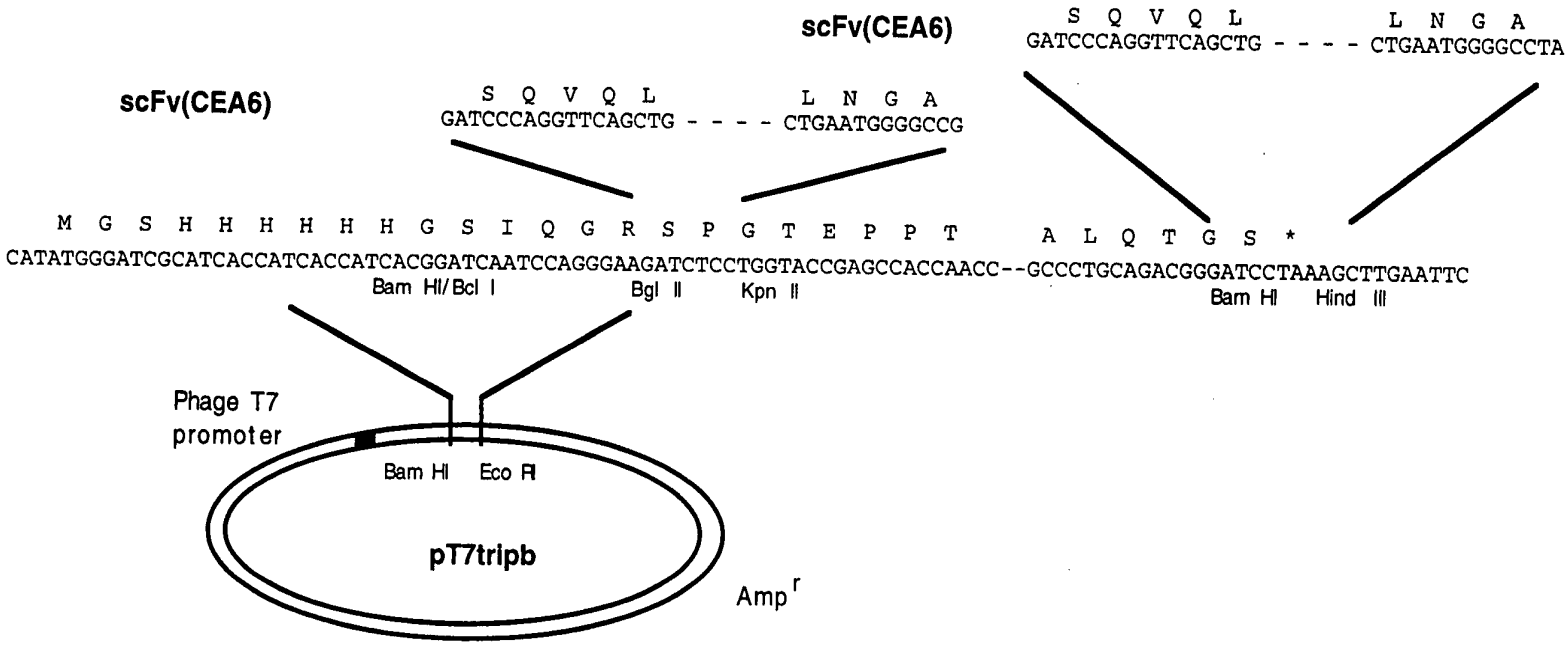
scFv(CEA6)
S Q V Q L
GATCCCAGGTTCAGCTG - - - - CTGAATGGGGCCG
L N G A
scFv(CEA6)
S Q V Q L
GATCCCAGGTTCAGCTG - - - - CTGAATGGGGCCTA
L N G A
M G S H H H H H H G S I Q G R S P G T E P P T A L Q T G S *
CATATGGGATCGCATCACCATCACCATCACGGATCAATCCAGGGAAGATCTCCTGGTACCGAGCCACCAACC--GCCCTGCAGACGGGATCCTAAAGCTTGAATTC
Bam HI/Bcl I
Bgl II
Kpn II
Bam HI
Hind III
Phage T7
promoter
Bam HI
Eco RI
pT7tripb
Amp r

Fig. 19

H6FXscFv(CEA6)-tripb-scFv(CEA6) fusion protein

```
  1 M G S H H H H H H G S I Q G R S Q V Q L Q Q S G A E V K K P  30
 31 G S S V K V S C K A S G G T F S N S P I N W L R Q A P G Q G  60
 61 L E W M G S I I P S F G T A N Y A Q K F Q G R L T I T A D E  90
 91 S T S T A Y M E L S S L R S E D T A V Y Y C A G R S H N Y E 120
121 L Y Y Y Y M D V W G Q G T M V T V S S G G G G S G G G G S G 150
151 G G G S D I Q M T Q S P S T L S A S I G D R V T I T C R A S 180
181 E G I Y H W L A W Y Q Q K P G K A P K L L I Y K A S S L A S 210
211 G A P S R F S G S G S G T D F T L T I S S L Q P D D F A T Y 240
241 Y C Q Q Y S N Y P L T F G G G T K L E I K R A A A E Q K L I 270
271 S E E D L N G A G T E P P T Q K P K K I V N A K K D V V N T 300
301 K M F E E L K S R L D T L A Q E V A L L K E Q Q A L Q T G S 330
331 Q V Q L Q Q S G A E V K K P G S S V K V S C K A S G G T F S 360
361 N S P I N W L R Q A P G Q G L E W M G S I I P S F G T A N Y 390
391 A Q K F Q G R L T I T A D E S T S T A Y M E L S S L R S E D 420
421 T A V Y Y C A G R S H N Y E L Y Y Y Y M D V W G Q G T M V T 450
451 V S S G G G G S G G G G S G G G G S D I Q M T Q S P S T L S 480
481 A S I G D R V T I T C R A S E G I Y H W L A W Y Q Q K P G K 510
511 A P K L L I Y K A S S L A S G A P S R F S G S G S G T D F T 540
541 L T I S S L Q P D D F A T Y Y C Q Q Y S N Y P L T F G G G T 570
571 K L E I K R A A A E Q K L I S E E D L N G A * 592
```

Fig. 20

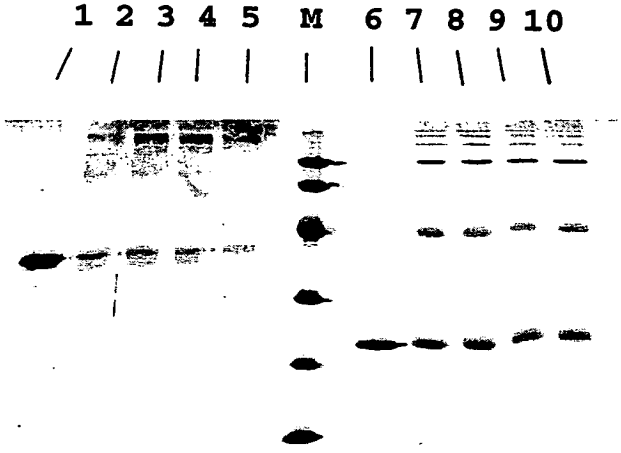

Fig. 21